

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 21:14:50 ; Search time 18.1938 Seconds
(without alignments)
6148.496 Million cell updates/sec

Title: US-09-099-823-1
Perfect score: 236
Sequence: 1 GACGCCCACTGACTGCCGA.....GCGGTGGGAAGTTGGGAAGSC 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- ```

Published: Applications NA:*
 : /cgn2_5/ptodata/1/pubnpa/US07_PUBCOMB.seq:*
 : /cgn2_5/ptodata/1/pubnpa/PCCT_NEW_PUB.seq:*
 : /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq:*
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 : /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq:*
 : /cgn2_6/ptodata/1/pubnpa/US06_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result<br>No. | Score | Query<br>Match | Length | DB | ID                  | SUMMARIES         |             |
|---------------|-------|----------------|--------|----|---------------------|-------------------|-------------|
|               |       |                |        |    |                     |                   | Description |
| 1             | 236   | 100.0          | 236    | 10 | US-09-099-823-1     | Sequence 1, Appli |             |
| 2             | 236   | 100.0          | 692    | 10 | US-09-099-823-4     | Sequence 4, Appli |             |
| 3             | 236   | 100.0          | 692    | 10 | US-09-099-823-5     | Sequence 5, Appli |             |
| 4             | 234   | 94.9           | 336    | 10 | US-09-833-381-1747  | Sequence 1, Appli |             |
| 5             | 196.4 | 83.2           | 523    | 10 | US-09-951-845-1     | Sequence 1, Appli |             |
| 6             | 134   | 52.5           | 245    | 10 | US-09-099-823-2     | Sequence 2, Appli |             |
| 7             | 35.8  | 15.2           | 2379   | 10 | US-09-815-243-7868  | Sequence 7868, Ap |             |
| 8             | 35.2  | 14.9           | 320    | 10 | US-09-923-876-3670  | Sequence 3670, Ap |             |
| 9             | 35    | 14.8           | 525    | 10 | US-09-374-671-1     | Sequence 1, Appli |             |
| 10            | 34.8  | 14.7           | 487    | 10 | US-09-864-761-26145 | Sequence 26145, A |             |
| 11            | 34.2  | 14.7           | 958    | 10 | US-09-864-761-9773  | Sequence 9773, Ap |             |
| c             | 34.1  | 14.5           | 600    | 10 | US-09-770-149-978   | Sequence 978, Ap  |             |
| 12            | 34.2  | 14.5           | 609    | 10 | US-09-770-149-885   | Sequence 885, App |             |
| 13            | 34.2  | 14.5           | 609    | 10 | US-09-886-055-194   | Sequence 194, App |             |
| c             | 34    | 14.4           | 948    | 10 | US-09-738-626-1278  | Sequence 1278, Ap |             |
| 15            | 33.6  | 14.2           | 2196   | 9  | US-09-963-790A-1    | Sequence 1, Appli |             |
| 16            | 33.6  | 14.2           | 2381   | 10 | US-09-838-785-1     | Sequence 1, Appli |             |
| 17            | 33    | 14.0           | 3320   | 10 | US-09-233-880-110   | Sequence 110, App |             |
| 18            | 33    | 14.0           | 3410   | 9  | US-09-015-896-110   | Sequence 110, App |             |
| 19            | 33    | 14.0           | 3410   | 9  | US-10-015-896-110   | Sequence 110, App |             |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                    |                   |                   |                   |                  |                   |                    |                     |                     |                    |                  |                    |                    |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|------------------|-------------------|--------------------|---------------------|---------------------|--------------------|------------------|--------------------|--------------------|
| 20                | 21                | 22                | 23                | 24                | 25                | 26                | 27                | 28                | 29                | 30                | 31                | 32                | 33                | 34                 | 35                | 36                | 37                | 38               | 39                | 40                 | 41                  | 42                  | 43                 | 44               | 45                 |                    |
| US-09-895-793-110 | US-09-895-814-110 | US-09-745-288-110 | US-09-759-143-110 | US-09-780-169-110 | US-09-030-606-110 | US-09-822-827-110 | US-09-115-453-110 | US-10-012-896-704 | US-09-895-793-704 | US-09-895-814-704 | US-09-759-143-704 | US-09-780-169-704 | US-09-822-827-704 | US-09-030-606-1591 | US-09-887-576-645 | US-09-764-864-764 | US-09-416-384-4   | US-09-416-384-4  | US-09-745-288-2   | US-09-960-352-403  | US-09-960-352-3496  | US-09-960-352-12483 | US-09-960-352-6549 | US-09-416-384A-1 | US-09-416-384A-4   | US-09-745-288-4034 |
| Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 110, App | Sequence 704, App | Sequence 704, App | Sequence 704, App | Sequence 704, App | Sequence 704, App | Sequence 1591, App | Sequence 645, App | Sequence 764, App | Sequence 349, App | Sequence 2, Appl | Sequence 403, App | Sequence 3496, App | Sequence 12483, App | Sequence 6549, App  | Sequence 1, Appl   | Sequence 4, Appl | Sequence 4034, App |                    |

## ALIGNMENTS

```

RESULT 1
US-09-099-823-1
; Sequence 1, Application US/09099823
; Patent No. US20020018990A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: KUSSELL, JOHN C.
; APPLICANT: SCHEFFEL, CHRISTI
; APPLICANT: STROUPE, STEPHEN D.
; APPLICANT: XU, HONG
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE BREAT
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,823
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,354
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.

```





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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 19:57:40 ; Search time 86.7066 seconds  
(without alignments)  
6129.540 Million cell updates/sec

Title: US-09-099-823-1  
Perfect score: 236  
Sequence: 1 GAGCCGAGTACGACGCGA.....GCGGTGGAGTGGAGCC 236

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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22: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID32/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 236   | 100.0       | 236    | 20 AAX07453 | Human BS124 specif |
| 2          | 236   | 100.0       | 690    | 21 AAZ91770 | Human breast speci |
| 3          | 236   | 100.0       | 692    | 20 AAX07456 | Human BS124 specif |
| 4          | 236   | 100.0       | 692    | 20 AAX07457 | Human BS124 specif |
| 5          | 236   | 100.0       | 738    | 22 AAF54313 | DNA encoding prote |
| 6          | 236   | 100.0       | 739    | 21 AAC58615 | Human PRO1283 prot |
| 7          | 236   | 100.0       | 739    | 21 AAZ37071 | Human PRO1283 (UNQ |
| 8          | 236   | 100.0       | 739    | 24 ABL95663 | Human angiotensin  |
| 9          | 236   | 100.0       | 739    | 24 ABL88174 | Human PRO1283 cDNA |

|    |       |      |       |             |                    |
|----|-------|------|-------|-------------|--------------------|
| 10 | 234   | 99.2 | 676   | 22 AAF80043 | Nucleotide sequenc |
| 11 | 234   | 99.2 | 782   | 22 AAF80044 | Nucleotide sequenc |
| 12 | 232.4 | 98.5 | 676   | 22 AAF80039 | Nucleotide sequenc |
| 13 | 232.4 | 98.5 | 725   | 22 AAF80040 | Nucleotide sequenc |
| 14 | 232.4 | 98.5 | 741   | 22 AAF80041 | Nucleotide sequenc |
| 15 | 224.6 | 95.2 | 357   | 21 AAC03580 | Human secreted pro |
| 16 | 214.4 | 90.8 | 781   | 22 AAK51815 | Human polynucleoti |
| 17 | 196.4 | 83.2 | 522   | 20 AAX19505 | Human lipocalin ho |
| 18 | 196.4 | 83.2 | 522   | 24 AAX35179 | Human 21lipol DNA. |
| 19 | 192   | 81.4 | 603   | 23 AAS76054 | DNA encoding novel |
| 20 | 190.4 | 80.7 | 666   | 23 AAS76055 | DNA encoding novel |
| 21 | 185   | 78.4 | 1002  | 20 AAV08842 | Gene No. 32 encodi |
| 22 | 166   | 70.3 | 981   | 20 AAV08845 | Gene No. 32 encodi |
| 23 | 136.6 | 57.9 | 510   | 20 AAX19506 | Degenerate lipocal |
| 24 | 124   | 52.5 | 245   | 20 AAX07454 | Human BS124 specif |
| 25 | 120.4 | 51.0 | 3952  | 22 AAL03258 | Human reproductiv  |
| 26 | 120.4 | 51.0 | 3955  | 22 AAL03257 | Human reproductiv  |
| 27 | 120.4 | 51.0 | 13391 | 22 AAF80047 | Nucleotide sequenc |
| 28 | 118.8 | 50.3 | 10664 | 22 AAF80046 | Nucleotide sequenc |
| 29 | 114   | 48.3 | 542   | 22 AAF80045 | Nucleotide sequenc |
| 30 | 114   | 48.3 | 607   | 22 AAF80042 | DNA encoding novel |
| 31 | 54.8  | 23.2 | 3348  | 23 AAS70271 | DNA encoding novel |
| 32 | 54.8  | 23.2 | 3348  | 23 AAS73851 | DNA encoding novel |
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| 35 | 54.8  | 23.2 | 3348  | 23 AAS81386 | DNA encoding novel |
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| 39 | 54.8  | 23.2 | 3349  | 23 AAS79120 | DNA encoding novel |
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| 41 | 52    | 22.0 | 52    | 20 AAX19514 | Human lipocalin ho |
| 42 | 52    | 22.0 | 770   | 20 AAX76463 | cDNA corresponding |
| 43 | 50    | 21.2 | 50    | 21 AAC58498 | Human PRO1283 (UNQ |
| 44 | 50    | 21.2 | 50    | 21 AAX37212 | Human PRO1283 hybr |
| 45 | 50    | 21.2 | 50    | 22 AAF54318 | Probe #25 used in  |

ALIGNMENTS

RESULT 1  
AAX07453  
ID AAX07453 standard; cDNA; 236 BP.  
XX  
AC AAX07453;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Human BS124 specific EST clone I730294.  
XX  
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
XX  
KW EST; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9859049-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-US12862.  
XX  
PR 20-JUN-1997; 97US-0879354.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;  
XX  
PI Gordon J, Granados EN, Hodges SC, Klass MF, Kratochvil JD;  
XX  
PI Russell JC, Scheffel CP, Stroupe SD, Yu H;  
XX  
DR WPI; 1999-105623/09.  
XX  
XX New isolated BS124 polynucleotides and polypeptides - used for



PT detecting, diagnosing, preventing or treating diseases or conditions  
 PT of the breast, such as breast cancer  
 XX Claim 11; Page 94; 125pp; English.  
 XX The sequence is that of a BS124-specific EST clone.  
 CC It is useful for detecting, diagnosing, staging, preventing  
 CC or treating, or determining predisposition to diseases or  
 CC conditions of the breast, such as breast cancer.  
 XX Sequence 236 BP; 47 A; 63 C; 86 G; 40 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 236; DB 20; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-51;  
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACCCGACGTGACCTGCGAGGTGCGGACGACAGACTCTGGAGATGAAGACCTGTTC 60  
 Db 1 GACCCGACGTGACCTGCGAGGTGCGGACGACAGACTCTGGAGATGAAGACCTGTTC 60  
 QY 61 TGGGTGTACAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
 Db 61 TGGGTGTACAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
 QY 121 CAGGACCTGTGTACGTGAAGCCCATGTGTGTGATGAAGACTTCCGGAGGACAGGAGGC 180  
 Db 121 CAGGACCTGTGTACGTGAAGCCCATGTGTGTGATGAAGACTTCCGGAGGACAGGAGGC 180  
 QY 181 CCAGGAAGTGTCTCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236  
 Db 181 CCAGGAAGTGTCTCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236  
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 AA291770  
 TD AA291770 standard; DNA; 690 BP.  
 AC AA291770;  
 XX 01-JUN-2000 (first entry)  
 DE Human breast specific gene IS clone 1213903.  
 KW Human; breast specific gene; breast specific marker; BSG; diagnosis;  
 KW breast cancer; therapy; ss.  
 XX Homo sapiens.  
 OS WO200008210-A1.  
 PN 17-FEB-2000.  
 PD 22-JUL-1999; 99WO-US16811.  
 PF 04-AUG-1998; 98US-0095232.  
 PR (DIAD-) DIADEXUS LLC.  
 PA Sun Y, Recipon H, Cafferkey R;  
 PI WPI; 2000-205737/18.  
 DR Detecting, diagnosing, monitoring, staging, prognosticating, imaging  
 PT and treating breast cancer using protein product of breast specific  
 PT genes -  
 XX Example 1; Page 43; 45pp; English.  
 XX This sequence represents a breast specific gene (BSG) clone. The BSG  
 CC sequences are also referred to as breast specific markers (BSM). The  
 CC invention relates to methods for diagnosing, monitoring, staging, imaging  
 CC and treating breast cancer (BC). The methods comprise measuring the  
 CC levels of BSG products in cells, tissues or body fluids of the patient

CC and comparing the measured levels of BSG, with BSG levels of a normal  
 CC human control. An antibody against the BSG sequences can be labelled and  
 CC used for imaging BC in a patient. The antibody can be conjugated to a  
 CC cytotoxic agent, and used for treating BC in a patient.  
 XX Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 236; DB 21; Length 690;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-51;  
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 GACCCGACGTGACCTGCGAGGTGCGGACGACAGACTCTGGAGATGAAGACCTGTTC 60  
 QY 61 TGGGTGTACAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
 Db 61 TGGGTGTACAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
 QY 121 CAGGACCTGTGTACGTGAAGCCCATGTGTGTGATGAAGACTTCCGGAGGACAGGAGGC 180  
 Db 121 CAGGACCTGTGTACGTGAAGCCCATGTGTGTGATGAAGACTTCCGGAGGACAGGAGGC 180  
 QY 181 CCAGGAAGTGTCTCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236  
 Db 181 CCAGGAAGTGTCTCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCC 236  
 RESULT 3  
 AA07456  
 TD AA07456 standard; cDNA; 692 BP.  
 AC AA07456;  
 XX 08-JUN-1999 (first entry)  
 DE Human BS124 specific EST clone 1730294IH.  
 KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
 KW EST; ss.  
 XX Homo sapiens.  
 OS WO9859049-A1.  
 PN 30-DEC-1998.  
 PD 19-JUN-1998; 98WO-US12862.  
 PF 20-JUN-1997; 97US-0879354.  
 PR (ABSO ) ABBOTT LAB.  
 PA Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;  
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
 PI Russell JC, Scheffel CP, Stroupe SD, Yu H;  
 PI WPI; 1999-105623/09.  
 DR New isolated BS124 polynucleotides and polypeptides - used for  
 PT detecting, diagnosing, preventing or treating diseases or conditions  
 PT of the breast, such as breast cancer  
 XX Claim 11; Pages 94-95; 125pp; English.  
 CC The sequence is that of a BS124-specific EST clone.  
 CC It is useful for detecting, diagnosing, staging, preventing  
 CC or treating, or determining predisposition to diseases or  
 CC conditions of the breast, such as breast cancer.  
 XX Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 236; DB 20; Length 692;





Query Match 32.3%; Score 76.2; DB 4; Length 147;  
Best Local Similarity 96.3%; Pred. No. 1.3e-11;  
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 84 GCTGCTCTGCTCTTACCTGAGGAGGAGGATATCACAGGACCTGTGACGTGAAGGCC 143

DB 67 GGTGCTCTGCTCTTACCTGAGGAGGAGGATATCACAGGACCTGTGACGTGAAGGCC 126

QY 144 ATGTGCTGTGATAGGACTTT 164

DB 127 ATGTGCTGTGATAGGACTTT 147

## RESULT 13

US-09-130-663-15/c  
; Sequence 15, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer: ZC13764  
US-09-130-663-15

Query Match 22.0%; Score 52; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 GGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGGTGTGCGATAAG 158

DB 52 GGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGGTGTGCGATAAG 1

## RESULT 14

US-09-432-335-15/c  
; Sequence 15, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; EARLIER FILING DATE: 1998-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer: ZC13764  
US-09-432-335-15

Query Match 22.0%; Score 52; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 GGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGGTGTGCGATAAG 158

DB 52 GGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGGTGTGCGATAAG 1

## RESULT 15

US-09-614-022-15/c  
; Sequence 15, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; EARLIER FILING DATE: 2000-07-11  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; NUMBER OF SEQ ID NOS: 30  
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US-09-614-022-15

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Search completed: February 9, 2003, 22:05:01  
Job time : 20.1542 secs



; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 ; FILE REFERENCE: 97-24  
 ; CURRENT APPLICATION NUMBER: US/09/432,335  
 ; CURRENT FILING DATE: 1999-11-02  
 ; EARLIER APPLICATION NUMBER: 09/130,663  
 ; EARLIER FILING DATE: 1998-08-06  
 ; EARLIER APPLICATION NUMBER: 60/054,867  
 ; EARLIER FILING DATE: 1997-08-06  
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 QY 99 ACCCTGGAGGAGGAGGATATCACAGGACCTGTGCTAGTGAAGCCCATGCTGTCGATAAG 158  
 DB 61 ACCCTGGAGGAGGAGGATATCACAGGACCTGTGCTAGTGAAGCCCATGCTGTCGATAAG 120  
 QY 159 GACTTTCCGAGGACAGAGGCCCCAGGAGGCTGTCCCAAGTGTCCCAAGTGTACAGCCCTGGGC 218  
 DB 121 GACTTTCCGAGGACAGAGGCCCCAGGAGGCTGTCCCAAGTGTCCCAAGTGTACAGCCCTGGGC 180  
 QY 219 GGTGGGAAGTTGGAAGCC 236  
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 US-09-614-022-1  
 ; Sequence 1, Application US/09614022  
 ; Patent No. 6385716  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Darrell C.  
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 ; FILE REFERENCE: 97-24  
 ; CURRENT APPLICATION NUMBER: US/09/614,022  
 ; CURRENT FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 09/130,663  
 ; PRIOR FILING DATE: 1998-08-06  
 ; PRIOR APPLICATION NUMBER: 60/054,867  
 ; PRIOR FILING DATE: 1997-08-06  
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RESULT 4  
 US-09-130-663-5  
 ; Sequence 5, Application US/09130663A  
 ; Patent No. 6020163  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Darrell C.  
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 ; FILE REFERENCE: 97-24  
 ; CURRENT APPLICATION NUMBER: US/09/130,663A  
 ; CURRENT FILING DATE: 1998-08-05  
 ; EARLIER APPLICATION NUMBER: 60/054,867  
 ; EARLIER FILING DATE: 1997-08-06  
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 ; SEQ ID NO 5  
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 ; TYPE: DNA  
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 ; NAME/KEY: variation  
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 ; Sequence 5, Application US/09432335  
 ; Patent No. 6143720  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Darrell C.  
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 ; FILE REFERENCE: 97-24  
 ; CURRENT APPLICATION NUMBER: US/09/432,335  
 ; CURRENT FILING DATE: 1999-11-02  
 ; EARLIER APPLICATION NUMBER: 09/130,663  
 ; EARLIER FILING DATE: 1998-08-06



















GenCore version 5.1.3  
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(without alignments)  
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Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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| 2         | 236   | 100.0       | 739    | 6     | AX491098 Sequence |
| 3         | 234   | 99.2        | 739    | 6     | AX083544 Sequence |
| 4         | 234   | 99.2        | 739    | 6     | AX083544 Sequence |
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| 12        | 232.4 | 98.5        | 739    | 6     | AX083536 Sequence |
| 13        | 196.4 | 83.2        | 522    | 6     | AX083540 Sequence |
| 14        | 196.4 | 83.2        | 522    | 6     | AX083540 Sequence |
| 15        | 136.6 | 57.9        | 510    | 6     | AX083551 Sequence |
| 16        | 120.4 | 51.0        | 13591  | 6     | AX083551 Sequence |
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ALIGNMENTS

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DEFINITION Sequence 205 from Patent WO0208284.  
ACCESSION AX454620  
VERSION AX454620.1 GI:21713934  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Baker, K.P., Ferrara, N., Gerber, H., Gertsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephanou, J.F., Watanabe, C.K., Williams, P.N., Wood, W.I.







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Best Local Similarity 100.0%; Pred. No. 3.5e-41;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
human.
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 676)
Pitiot, G., Lacazette, E., and Gachon, P.
Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
Patent: WO 0112806-A 1 22-FEB-2001;
Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)
JOURNAL
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 676)
Lacazette, E., Gachon, A.M. and Pitiot, G.
A novel human odorant-binding protein gene family resulting from
genomic duplicons at 9q34: differential expression in the oral and
genital spheres
Hum. Mol. Genet. 9 (2), 289-301 (2000)
JOURNAL
MEDLINE
20076326
PUBMED
10607840
REFERENCE
2 (bases 1 to 676)
Gachon, A.M.
Direct Submission
TITLE
Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri
Dunant, Clermont Ferrand cedex 01 63001, FRANCE
JOURNAL
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Best Local Similarity 99.6%; Pred. No. 7.9e-41;
Matches 233; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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SOURCE human.  
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.  
TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
polypeptides and polynucleotides coding for said polypeptides and  
uses thereof  
JOURNAL Patent: WO 0112806-A 5 22-FEB-2001;  
Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)  
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ACCESSION A3251024.1 GI:6900072  
VERSION A3251024.1  
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SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Lacazette, E., Gachon, A.M. and Pitiot, G.  
TITLE A novel human odorant-binding protein gene family resulting from  
genomic duplications at 9q34: differential expression in the oral and  
genital spheres  
JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)  
MEDLINE 20076326  
PUBMED 10607840  
REFERENCE 2 (bases 1 to 741)  
AUTHORS Gachon, A.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM

U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
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DB 181 AGGAAGTGTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 234  
RESULT 13  
AR204078 522 bp DNA linear PAT 20-JUN-2002  
LOCUS Sequence 1 from patent US 6365716.  
DEFINITION  
ACCESSION AR204078  
VERSION AR204078.1 GI:21500632  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 522)  
AUTHORS Conklin, D.C.  
TITLE Antibodies to lipocalin homologs  
JOURNAL Patent: US 6365716-A 1 02-APR-2002;  
FEATURES Location/Qualifiers  
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BASE COUNT 135 a 132 c 172 g 93 t  
ORIGIN  
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Best Local Similarity 99.5%; Pred. No. 5.4e-33;  
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 39 CTGAGATGAAGACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 98  
DB 1 CTGAGATGAAGACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60

QY 99 ACCCTGGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGCTGTCGATAAG 158  
Db 61 ACCCTGGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGCTGTCGATAAG 120  
QY 159 GACTTTCGGAGGACAGGAGCCAGGAAGGTGTCCCAAGTGAAGTGACAGCCCTGGGC 218  
Db 121 GACTTTCGGAGGACAGGAGCCAGGAAGGTGTCCCAAGTGAAGTGACAGCCCTGGGC 180  
QY 219 GGTGGGAAGTTGGAAGCC 236  
Db 181 GGTGGGAAGTTGGAAGCC 198

RESULT 14  
AX451327  
LOCUS AX451327 523 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 1 from Patent WO223201.  
ACCESSION AX451327  
VERSION AX451327.1 GI:21698379  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Lok S., Foster, D.C. and Holloway, J.L.  
TITLE Use of human pheromone polypeptides  
JOURNAL Patent: WO 023201-A.1 21-MAR-2002;  
ZymoGenetics, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..523  
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/db\_xref="taxon:9606"  
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/note="unnamed protein product"  
/codon\_start=1  
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/db\_xref="GI:21698380"  
/translation="MKTFLGVTLGLAALFTLEEDITGWTVMVVDKPPEDR  
RPRKVPKVTALGGKLEATFPMREDRCIOKILMRTEPKYSAYGGRKLMYIQ  
ELPRDEHYIFPKDQHGGLLENGKLVGRNSDTNREALPEFKLVQRKGLSEIDFTF  
LOTGSCVPEH"  
BASE COUNT 125 a 133 c 172 g 93 t

Query Match 83.2%; Score 196.4; DB 6; Length 523;  
Best Local Similarity 99.5%; Pred. No. 5,4e-33;  
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 39 CTGGAGTACAGACCTGTCTCGGTGTACCGCTGCGCTGCGCTGCGCTGCTTC 98  
Db 2 CTGAGATGAAGACCCCTTCTCGGTGTACCGCTGCGCTGCGCTGCGCTGCTTC 61  
QY 99 ACCCTGGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGCTGTCGATAAG 158  
Db 62 ACCCTGGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGCTGTCGATAAG 121  
QY 159 GACTTTCGGAGGACAGGAGCCAGGAAGGTGTCCCAAGTGAAGTGACAGCCCTGGGC 218  
Db 122 GACTTTCGGAGGACAGGAGCCAGGAAGGTGTCCCAAGTGAAGTGACAGCCCTGGGC 181  
QY 219 GGTGGGAAGTTGGAAGCC 236  
Db 182 GGTGGGAAGTTGGAAGCC 199

RESULT 15  
AR204081  
LOCUS AR204081 510 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 5 from patent US 6365716.  
ACCESSION AR204081  
VERSION AR204081.1 GI:21500636  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 510)  
AUTHORS Conklin, D.C.  
TITLE Antibodies to lipocalin homologs  
JOURNAL Patent: US 6365716-A 02-APR-2002;  
FEATURES Location/Qualifiers  
source 1..510  
/organism="unknown"  
BASE COUNT 99 a 44 c 95 g 66 t 206 others  
ORIGIN

Query Match 57.9%; Score 136.6; DB 6; Length 510;  
Best Local Similarity 60.7%; Pred. No. 5.3e-20;  
Matches 116; Conservative 35; Mismatches 40; Indels 0; Gaps 0;  
QY 45 ATGAAGACCTGTCTCGGTGTACCGCTGCGCTGCGCTGCTTCACCTG 104  
Db 1 ATGAAGACCTGTCTCGGTGTACCGCTGCGCTGCGCTGCTTCACCTG 60  
QY 105 GAGGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGCTGTCGATAAGGACTTT 164  
Db 61 GAGGAGGAGGATATCACAGGACCTGTGACGTGAAGCCATGCTGTCGATAAGGACTTT 120  
QY 165 CCGGAGGAGGAGGAGCCAGGAAGGTGTCCCAAGTGAAGTGACAGCCCTGGCGTGG 224  
Db 121 CCGGAGGAGGAGGAGCCAGGAAGGTGTCCCAAGTGAAGTGACAGCCCTGGCGTGG 180  
QY 225 AAGTTCGAGCC 235  
Db 181 AAGTTCGAGCC 191

Search completed: February 10, 2003, 03:12:27  
Job time : 780.819 secs



;; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
;; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
;; NUMBER OF SEQUENCES: 27  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Abbott Laboratories  
;; STREET: 100 Abbott Park Road  
;; CITY: Abbott Park  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60064-3500  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/099,823  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/879,354  
;; FILING DATE: 20-JUN-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Becker, Cheryl L.  
;; REGISTRATION NUMBER: 35,441  
;; REFERENCE/DOCKET NUMBER: 6120.US.P1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 847/935-1729  
;; TELEFAX: 847/938-2623  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 245 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-09-099-823-2  
Query Match 52.5%; Score 124; DB 10; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 113 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGCATAGGACTTCCGGAGGA 172  
Db 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGCATAGGACTTCCGGAGGA 60  
QY 173 CAGGAGCCCGCAGGAGGTGTCCTCCAGTGAAGTGCACAGCCCTGGCGGTGGAGTTGGA 232  
Db 61 CAGGAGCCCGCAGGAGGTGTCCTCCAGTGAAGTGCACAGCCCTGGCGGTGGAGTTGGA 120  
QY 233 AGCC 236  
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RESULT 7  
US-09-815-242-7868  
; Sequence 7868, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Baselbeck, Robert  
; APPLICANT: Ohlson, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Cart, Grant J.  
; APPLICANT: Yamamoto, Robert F.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7868  
;; LENGTH: 2379  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)...(2379)  
US-09-815-242-7868  
Query Match 15.2%; Score 35.8; DB 10; Length 2379;  
Best Local Similarity 50.9%; Pred. No. 1.1;  
Matches 85; Conservative 0; Mismatches 82; Indels 0; Gaps 0;  
QY 9 GTGACCTGCGCGAGGTGCGGACGACGAGCTCTGGAGATGAAGACCTCTTCTGGGTGTC 68  
Db 55 GCGTCTTGGCGCGCGCGGTGTGGAAGAGCTGCCCGGGTGGCGCGGCC 114  
QY 69 AGCTCGCGCGTGGCGCGCTGCTCTTACCTCGAGGAGGAGGATATCACAGGAGCC 128  
Db 115 TCGGTCAACTGGCCAGCGAGCGAGCGCGCTACAGGCGCGCGCGGCGGCGCTGCCGCGCC 174  
QY 129 TGGTACGTGAAGGCATGTGTGATGAAGGACTTTCGGAGGACAG 175  
Db 175 CTGTGTGCGCGGTGTCAGCAGCGCGCTACAGGTTCGGCGCGCGAG 221  
RESULT 8  
US-09-923-876-3670  
; Sequence 3670, Application US/09923876  
; Patent No. US20020013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Kamigaki, Laura Y. (Ito)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 3670  
; LENGTH: 320  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700405401H1  
; NAME/KEY: unsure  
; LOCATION: 99  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-3670  
Query Match 14.9%; Score 35.2; DB 10; Length 320;





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/ OTHER INFORMATION: MAP TO AL008723.8
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL 2.4
/ OTHER INFORMATION: EXPRESSED IN FETTERPIT, SIGNAL 1.8
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
/ OTHER INFORMATION: EST HIR: g15548724, EVALUE 0.06+00
/ OTHER INFORMATION: SWT HUMAN HIR: BF348283.1 EVALUES 0.00e+00
/ OTHER INFORMATION: SWISSPROT HIT: Q10570, EVALUAE 1.00e-52
US-09-864-761-26145

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| Query Match           | 14.7%                                                              | Score 34.8;    | DB 10;    | Length 487; |
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| Db                    |                                                                    |                |           |             |
| QY 237                | CGCTCAGCAAGGAGAACCGAGGTACAGCTTCAAAGGCTACGCTGTGGTCCCGCGGCACTGCC 296 |                |           |             |
| Db                    |                                                                    |                |           |             |
| QY 97                 | TCACCTGGAGGAGGAGATATCAGAGGACCTGTGTAGGTGAAGGCCCATGTGGTGTGATA 156    |                |           |             |
| Db                    |                                                                    |                |           |             |
| QY 297                | TCATCGAGGAGGAGGAGGATCATGTCTGAGGGCGGATCTTGTATCATGGATGTGACTG 356     |                |           |             |
| Db                    |                                                                    |                |           |             |
| QY 157                | AGSACTTTCGGAGGACAGGAGGCCACAGA 186                                  |                |           |             |
| Db                    |                                                                    |                |           |             |
| QY 357                | AGGTGTGCCCGAGCCAGCCAGCCCTTGA 386                                   |                |           |             |
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RESULT 11  
US-09-864-761-9773  
Sequence 9773, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aseomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661

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; PRIOR FILLING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCI/US01/00670
; PRIOR FILLING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILLING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILLING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILLING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9773
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL008723.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEPAT, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-9773

Query Match 14.7%; Score 34.8; DB 10; Length 958;
Best Local Similarity 52.0%; Pred. No. 1.7;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps

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Db 618 CGCTCAGCAGGAGACAGGTCAGGCTTCAAGAGCTACGGTGGCCGCCGGAAGCTGCC 9773
 |||||

QY 97 TCACCTGGAGGAGGAGATATCATCAGGACCTGCTGTAAGTGAAGGCATGTGGTGCATA 156
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Db 678 TCATCAGGAGGAGGAGGAGGTGATGCTCTCAGGCGCGGATCTTGTATCATGATGTGACTG 737
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QY 157 AGGACTTTCGGAGCAGCAGGAGGCCAGGA 186
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Db 738 AGGTGGTGCCCGAGCCAGCAGCAGCCCTTGA 767
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RESULT 12
US-09-770-149-978/c
 / Sequence 978, Application US/09770149
 / Patent No. US2002005963A1
 / GENERAL INFORMATION:
 / APPLICANT: Goralch, Qiang
 / APPLICANT: An, Yong-Qiang
 / APPLICANT: Hamilton, Carol M.
 / APPLICANT: Price, Jennifer L.
 / APPLICANT: Raines, Tracy M.
 / APPLICANT: Yu, Yang
 / APPLICANT: Rameaka, Joshua G.
 / APPLICANT: Page, Amy
 / APPLICANT: Matthew, Abraham V.
 / APPLICANT: Ledford, Brooke L.
 / APPLICANT: Woessner, Jeffrey P.
 / APPLICANT: Haas, William David
 / APPLICANT: Garcia, Carlos A.
 / APPLICANT: Kricker, Maja
 / APPLICANT: Slader, Ted
 / APPLICANT: Davis, Keith R.
 / APPLICANT: Allen, Keith
 / APPLICANT: Hoffman, Neil
 / APPLICANT: Huban, Patrick
 / TITLE OF INVENTION: Expressed Sequences of Arabidopsis
 / TITLE OF INVENTION: thaliana
 / FILE REFERENCE: 2024 (PARA-013PRV)
 / CURRENT APPLICATION NUMBER: US/09/770.149
 / CURRENT FILING DATE: 2001-01-26

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; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ. IDS NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1278
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1278

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| Query Match           | 14.2%;                                                     | Score 33.6;    | DB 9;     | Length 2196; |
|-----------------------|------------------------------------------------------------|----------------|-----------|--------------|
| Best Local Similarity | 51.3%;                                                     |                |           |              |
| Matches 78;           | Conservative 0;                                            | Mismatches 74; | Indels 0; | Gaps 0;      |
| QY 68                 | CACGTCGCCTGGCCGCTGCTCTTCACCTCGAGGAGGAGGATATCACAGGAC        | 127            |           |              |
| DB 2041               | CBCGCTGCAGCTGGACGTGACCGTGCAGATCTGGAACCGCTGGAGCTTTCCGCGGTGA | 2100           |           |              |
| QY 128                | CTGTACTGTGAAGGCATGTGTGCTCGATAAGCACTTTCCGAGGACAGGAGCCCCAGAA | 187            |           |              |
| DB 2101               | CGTGACCGTGATGATCTGTGCAGCAGCGGTGTGATTCGCGGACGACGACCGCGGAGAC | 2160           |           |              |
| QY 188                | GGTGTCCCCAGTGAAGTGACAGCCCTGGGCG                            | 219            |           |              |
| DB 2161               | CGTGTGGCCGTGGCGGTTACCGTGGCGGAQG                            | 2192           |           |              |

Search completed: February 9, 2003, 22:08:13  
Job time : 24.1938 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: February 9, 2003, 22:05:30 ; Search time 656.018 seconds  
(without alignments)  
5826.269 Million cell updates/sec

Title: US-09-099-823-1

Perfect score: 236  
Sequence: 1 GAGGCCAGTGCCTGCCGA.....GCGGTGGGAATTTGGAAGCC 236

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hic.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hic.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pin.\*

21: em\_gss\_vrt.\*

22: em\_gss\_fun.\*

23: em\_gss\_man.\*

24: em\_gss\_mus.\*

25: em\_gss\_other.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
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| 1          | 94.6  | 40.1        | 337    | 12    | BF193883 245614 WA |
| 2          | 68.8  | 29.2        | 494    | 14    | R47029 Y358 Rat in |
| 3          | 58.4  | 24.7        | 603    | 10    | BB618259 BB618259  |
| 4          | 57.2  | 24.2        | 519    | 9     | AI877465 udl0d09.i |
| 5          | 51.8  | 21.9        | 532    | 10    | AW513637 x047h10.x |
| 6          | 50.4  | 21.4        | 626    | 10    | BB028765 BB028765  |

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| c | 8  | 41.6 | 17.6 | 594 | 10 | AW920286 |
| c | 9  | 41.4 | 17.5 | 753 | 9  | AL567433 |
| c | 10 | 41   | 17.4 | 955 | 12 | BG493366 |
| c | 11 | 39.2 | 16.6 | 512 | 14 | BQ821423 |
| c | 12 | 39.2 | 16.6 | 597 | 10 | BE337290 |
| c | 13 | 39.2 | 16.6 | 627 | 10 | BE212139 |
| c | 14 | 39.2 | 16.6 | 629 | 10 | BE452872 |
| c | 15 | 39.2 | 16.6 | 645 | 14 | BQ818346 |
| c | 16 | 39.2 | 16.6 | 654 | 13 | BI997395 |
| c | 17 | 39.2 | 16.6 | 666 | 12 | BG854372 |
| c | 18 | 39.2 | 16.6 | 666 | 12 | BG854590 |
| c | 19 | 39.2 | 16.6 | 674 | 12 | BG857733 |
| c | 20 | 39.2 | 16.6 | 685 | 12 | BG859756 |
| c | 21 | 39.2 | 16.6 | 694 | 12 | BG853153 |
| c | 22 | 39.2 | 16.6 | 694 | 12 | BE751079 |
| c | 23 | 39   | 16.5 | 561 | 12 | BE750496 |
| c | 24 | 39   | 16.5 | 581 | 13 | BI538748 |
| c | 25 | 38.8 | 16.4 | 468 | 12 | BE708258 |
| c | 26 | 38.8 | 16.4 | 537 | 12 | BE753611 |
| c | 27 | 38.4 | 16.3 | 471 | 13 | BI046625 |
| c | 28 | 37.8 | 16.0 | 575 | 17 | CN802FAE |
| c | 29 | 37.6 | 15.9 | 581 | 10 | BE251756 |
| c | 30 | 37.4 | 15.8 | 418 | 10 | AV639302 |
| c | 31 | 37.4 | 15.8 | 613 | 13 | BM488076 |
| c | 32 | 37.4 | 15.8 | 433 | 14 | N71534   |
| c | 33 | 37.2 | 15.8 | 527 | 10 | AW745759 |
| c | 34 | 37.2 | 15.8 | 710 | 13 | BJ319621 |
| c | 35 | 37   | 15.7 | 679 | 10 | AW947575 |
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| c | 37 | 36.4 | 15.4 | 611 | 13 | BI066117 |
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ACCESSION BF193883.1 GI:11077252  
VERSION BF193883.1  
KEYWORDS EST.  
SOURCE Bos taurus  
ORGANISM Bos taurus  
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 337)  
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
Perteira,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and  
Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine CDNA  
libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithfemail.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred





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ACCESSION AW513637  
 VERSION EST  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 532)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
 Tissue Procurement: Christopher Moskalek, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: [image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

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 VERSION BB028765.2 GI:16258092  
 KEYWORDS EST.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 626)  
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.

Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
 Unpublished (2001)  
 On Jun 8, 2000 this sequence version replaced gi:8383516.  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp,  
 URL:<http://genome.gsc.riken.go.jp/>  
 Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Imanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
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FEATURES  
 source













GenCore version 5.1.3  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 245   | 100.0       | 523    | 6     | AX451327 Sequence  |
| 3          | 245   | 100.0       | 676    | 6     | AX083544 Sequence  |
| 4          | 245   | 100.0       | 676    | 6     | AX251026 Homo sapi |
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| 7          | 240.2 | 98.0        | 676    | 6     | AX083536 Sequence  |
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6365716.  
ACCESSION AR204078  
VERSION AR204078.1 GI:21500632  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 522)  
AUTHORS Conklin,D.C.  
TITLE Antibodies to lipocalin homologs  
JOURNAL Patent: US 6365716-A 1 02-APR-2002;  
FEATURES Location/Qualifiers

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Mon Feb 10 11:11:43 2003

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DEFINITION Sequence 1 from Patent WO0223201.
ACCESSION AX451327
VERSION AX451327.1 GI:21698379
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lok, S., Foster, D.C. and Holloway, J.L.
TITLE Use of human pheromone polypeptides
JOURNAL Patent: WO 0223201-A 1 21-MAR-2002;
Zymogenetics, Inc. (US)
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DEFINITION Sequence 9 from Patent WO0112806.
ACCESSION AX083544
VERSION AX083544.1 GI:13185354
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.
TITLE Odorant-binding human proteins fixing hydrophobic ligands:
polypeptides and polynucleotides coding for said polypeptides and
uses thereof
JOURNAL Patent: WO 0112806-A 9 22-FEB-2001;
Universite d'Auvergne (FR); Pitiot, Gilles (FR)
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TITLE Compositions and methods for the diagnosis and treatment of

JOURNAL disorders involving angiogenesis

Genentech, Inc. (US)

Patent: WO 020690-A 205 03-JAN-2002;

Location/Qualifiers

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QY 61 CAGGAGCCCGCAGGAGGTGCCCCAGTGAAGTACAGCCCTGGGGCGTGGAAAGTTGA 120

DB 173 CAGGAGCCCGCAGGAGGTGCCCCAGTGAAGTACAGCCCTGGGGCGTGGAAAGTTGA 232

QY 121 AGCCAGCTTCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCCTGATGCGGAA 180

DB 233 AGCCAGCTTCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCCTGATGCGGAA 292

QY 181 GACGAGGAGCCTGGCAATACAGCGCCTATGGGGCGAGGAGCTCATGATGCGAGGA 240

DB 293 GACGAGGAGCCTGGCAATACAGCGCCTATGGGGCGAGGAGCTCATGATGCGAGGA 352

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DB 353 GCTGC 357

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AX083536

LOCUS Sequence 1 from Patent WO0112806.

ACCESSION AX083536

VERSION AX083536.1 GI:13185346

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.

TITLE Odorant-binding human proteins fixing hydrophobic ligands: polypeptides and polynucleotides coding for said polypeptides and uses thereof

JOURNAL Patent: WO 0112806-A 1 22-FEB-2001;

Univ. d'Auvergne (FR); Pitiot, Gilles (FR)

Location/Qualifiers

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Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 111 GGATATCACAGGACCTGGTGAAGCCATGGTGGTCGATGAAGGACTTTCGGAGGA 170

QY 61 CAGGAGCCCGCAGGAGGTGCCCCAGTGAAGTACAGCCCTGGGGCGTGGAAAGTTGA 120

DB 171 CAGGAGCCCGCAGGAGGTGCCCCAGTGAAGTACAGCCCTGGGGCGTGGAAAGTTGA 230

QY 121 AGCCAGCTTCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCCTGATGCGGAA 180

DB 231 AGCCAGCTTCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCCTGATGCGGAA 290

QY 181 GACGAGGAGCCTGGCAATACAGCGCCTATGGGGCGAGGAGCTCATGATGCGAGGA 240

DB 291 GACGAGGAGCCTGGCAATACAGCGCCTATGGGGCGAGGAGCTCATGATGCGAGGA 350

QY 241 GCTGC 245

DB 351 GCTGC 355

RESULT 8

HS251021

LOCUS Homo sapiens mRNA for putative odorant binding protein aa (OBPIIIA

gene).

ACCESSION AJ251021

VERSION AJ251021.1 GI:5900066

KEYWORDS OBPIIIA gene; odorant binding protein.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Lacazette, E., Gachon, A.M. and Pitiot, G.

TITLE A novel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres

JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)

REFERENCE 2 (bases 1 to 676)

Medline 20076326

PUBMED 10607840

AUTHORS Gachon, A.M.

TITLE Direct Submission

JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM

U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri

Dunant, Clermont Ferrand cedex 01 63001, FRANCE

Location/Qualifiers

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/gene="OBPIIIA"

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/protein\_id="CAE71318.1"

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BASE COUNT 158 a 199 c 204 g 115 t

ORIGIN

Query Match 98.0%; Score 240.2; DB 9; Length 676;

Best Local Similarity 98.8%; Pred. No. 1.1e-48;

Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



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 Db 111 GGATATCACAGGACCTGTGACGATGAGGCCATGTGTGATAGGACTTTCCGGAGGA 170  
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 Db 231 AGCCAGCTTCACCTTCATGAGGAGGATCGGTGCATCCAGAGAAATCTGATCGCGAA 290  
 QY 181 GACGAGGAGGCTTGGCAAAATACAGCGCTATGGGCGCAGGAAGCTCATGATCGAGGA 240  
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 QY 241 GCTGC 245  
 Db 351 GCTGC 355  
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 LOCUS Sequence 3 from Patent WO0112806.  
 DEFINITION  
 ACCESSION AX083538  
 VERSION AX083538.1 GI:13185348  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 725)  
 Pitiot, G., Lacazette, E. and Gachon, F.  
 Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 Patent: WO 0112806-A 3 22-FEB-2001;  
 Universite d'Auvergne (FR); Pitiot, Gilles (FR)  
 JOURNAL Location/Qualifiers  
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QY 241 GCTGC 245  
 Db 351 GCTGC 355  
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 LOCUS Homo sapiens mRNA for putative odorant binding protein ab (OBP11a  
 DEFINITION  
 ACCESSION AJ251022  
 VERSION AJ251022.1 GI:6900068  
 KEYWORDS OBP11a gene; odorant binding protein.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 725)  
 Lacazette, E., Gachon, A.M. and Pitiot, G.  
 A novel human odorant-binding protein gene family resulting from  
 genomic duplicons at 9q34: differential expression in the oral and  
 genital spheres  
 Hum. Mol. Genet. 9 (2), 289-301 (2000)  
 JOURNAL  
 MEDLINE 20076326  
 PUBMED 10607840  
 REFERENCE 2 (bases 1 to 725)  
 Gachon, A.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
 U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
 Dunant, Clermont Ferrand cedex01 63001, FRANCE  
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 BASE COUNT 163 a 222 c 217 g 123 t  
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 Query Match 98.0%; Score 240.2; DB 9; Length 725;  
 Best Local Similarity 98.8%; Pred. No. 1.1e-48;  
 Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGATATCACAGGACCTGTGACGATGAGGCCATGTGTGATAGGACTTTCCGGAGGA 60  
 Db 111 GGATATCACAGGACCTGTGACGATGAGGCCATGTGTGATAGGACTTTCCGGAGGA 170  
 QY 61 CAGGAGGCCAGGAAGGTGTCCTGAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGA 120  
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 QY 241 GCTGC 245



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 782)  
Pitiot,G., Lacazette,E. and Gachon,F.  
TITLE  
Odorant-binding human proteins fixing hydrophobic ligands:  
polypeptides and polynucleotides coding for said polypeptides and  
uses thereof

JOURNAL  
Patent: WO 01/2806-A 11 22-FEB-2001;  
Universite d'Auvergne (FR); Pitiot, Gilles (FR)

## FEATURES

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BASE COUNT 186 a 226 c 239 g 131 t  
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Query Match 85.3%; Score 209; DB 6; Length 782;  
Best Local Similarity 100.0%; Pred. No. 4.8e-41;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 14

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LOCUS  
DEFINITION  
Homo sapiens mRNA for putative odorant binding protein bb (OBPIIb  
gene).  
ACCESSION  
AJ251027  
VERSION  
AJ251027.1 GI:6900078  
KEYWORDS  
OBPIIb gene; odorant binding protein.  
SOURCE  
Homo sapiens  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
Lacazette,E., Gachon,A.M. and Pitiot,G.  
TITLE  
A novel human odorant-binding protein gene family resulting from  
genomic duplicons at 9q34: differential expression in the oral and  
genital spheres

JOURNAL  
Hum. Mol. Genet. 9 (2), 289-301 (2000)  
MEDLINE  
20076326  
PUBMED  
10607840

REFERENCE  
2 (bases 1 to 782)

GENBANK  
Gachon,A.M.

Direct Submission

TITLE  
Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
Dunant, Clermont Ferrand cedex01 63001, FRANCE  
JOURNAL  
FEATURES  
Location/Qualifiers

## source

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BASE COUNT 186 a 226 c 239 g 131 t  
ORIGIN

Query Match 85.3%; Score 209; DB 9; Length 782;  
Best Local Similarity 100.0%; Pred. No. 4.8e-41;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGGTACGTGAGCCCATGGTGGTGCATAGGACCTTCCGGAGGA 60  
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QY 181 GACGAGGAGCCTGGCAATACAGCGCT 209  
DB 291 GACGAGGAGCCTGGCAATACAGCGCT 319

## RESULT 15

AR204081 510 bp DNA linear PAT 20-JUN-2002  
LOCUS  
DEFINITION  
Sequence 5 from patent US 6365716.  
ACCESSION  
AR204081  
VERSION  
AR204081.1 GI:21500636  
KEYWORDS  
Unknown.  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.

REFERENCE  
1 (bases 1 to 510)  
AUTHORS  
Conklin,D.C.  
TITLE  
Antibodies to lipocalin homologs  
JOURNAL  
Patent: US 6365716-A 5 02-APR-2002;  
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Location/Qualifiers

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Best Local Similarity 61.6%; Pred. No. 3.4e-34;  
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DB 129 YKGMGNCNNGAARGTNSNCCNGTWARGNACNCNTNGNGNGNGNGNAARYTNGA 188



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 19:57:40 : Search time 90.0132 Seconds  
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Searched: 2185239 seqs, 112599159 residues

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- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 245         | 100.0 | 245    | 20 | AA07454 Human BS124 specif  |
| 2          | 245         | 100.0 | 522    | 20 | AA19505 Human lipocalin ho  |
| 3          | 245         | 100.0 | 523    | 24 | AA035179 Human 21lipol DNA  |
| 4          | 245         | 100.0 | 603    | 23 | AA076054 DNA encoding novel |
| 5          | 245         | 100.0 | 676    | 22 | AA080043 Nucleotide sequenc |
| 6          | 245         | 100.0 | 690    | 21 | AA031770 Human breast speci |
| 7          | 245         | 100.0 | 692    | 20 | AA07456 Human BS124 specif  |
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| 9          | 245         | 100.0 | 738    | 22 | AA054313 DNA encoding prote |

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| 10 | 245   | 100.0 | 739   | 21 | AA058615 Human PRO1283 prot  |
| 11 | 245   | 100.0 | 739   | 21 | AAA37071 Human PRO1283 (UNQ  |
| 12 | 245   | 100.0 | 739   | 24 | ABL95663 Human angiogenesis  |
| 13 | 245   | 100.0 | 739   | 24 | ABL81174 Human PRO1283 cDNA  |
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| 16 | 240.2 | 98.0  | 741   | 22 | AA080041 Nucleotide sequenc  |
| 17 | 240.2 | 98.0  | 781   | 22 | AA051815 Human polynucleoti  |
| 18 | 230.6 | 94.1  | 357   | 21 | AA035800 Human secreted pro  |
| 19 | 209.2 | 85.4  | 666   | 23 | AA076055 DNA encoding novel  |
| 20 | 209   | 85.3  | 782   | 22 | AA080044 Nucleotide sequenc  |
| 21 | 181   | 73.9  | 510   | 20 | AA019506 Degenerate lipocal  |
| 22 | 174.8 | 71.3  | 981   | 20 | AA080845 Gene No. 32 encodi  |
| 23 | 174.8 | 71.3  | 1002  | 20 | AA080842 Gene No. 32 encodi  |
| 24 | 136.6 | 55.8  | 3952  | 22 | AA032558 Human reproductive  |
| 25 | 136.6 | 55.8  | 3955  | 22 | AA032557 Human reproductive  |
| 26 | 136.6 | 55.8  | 13591 | 22 | AA080047 Nucleotide sequenc  |
| 27 | 135   | 55.1  | 10664 | 22 | AA080046 Nucleotide sequenc  |
| 28 | 124   | 50.6  | 236   | 20 | AA07453 Human BS124 specif   |
| 29 | 105.8 | 43.2  | 542   | 22 | AA080045 Nucleotide sequenc  |
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| 31 | 82    | 33.5  | 770   | 22 | AA076463 cDNA encoding novel |
| 32 | 77.2  | 31.5  | 2598  | 23 | AA093598 cDNA encoding novel |
| 33 | 70.4  | 28.7  | 525   | 15 | AA069950 cDNA encoding novel |
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| 36 | 51.4  | 21.0  | 3348  | 23 | AA075011 DNA encoding novel  |
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| 42 | 51.4  | 21.0  | 3349  | 23 | AA079120 DNA encoding novel  |
| 43 | 51.4  | 21.0  | 3855  | 23 | AA070614 DNA encoding novel  |
| 44 | 51.2  | 20.9  | 774   | 17 | AA035147 cDNA encoding VNSP  |
| 45 | 50    | 20.4  | 50    | 21 | AA058498 Human PRO1283 (UNQ  |

ALIGNMENTS

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XX  
DT 08-JUN-1999 (first entry)  
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XX  
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
KW EST; ss.  
XX  
OS Homo sapiens.  
XX  
PN W0859049-Al.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-US12862.  
XX  
PR 20-JUN-1997; 97US-0879354.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Billing-medell PA, Cohen M, Colpitts TL, Friedman PN;  
PI Gordon J, Granados RV, Hodges SC, Klass MR, Kratochvil JD;  
PI Russell JC, Scheffel CP, Stroupe SD, Yu H,  
XX  
DR WPI; 1999-105623/09.  
XX  
PT New isolated BS124 polynucleotides and polypeptides - used for

PT detecting, diagnosing, preventing or treating diseases or conditions  
PT of the breast, such as breast cancer  
XX  
PS Claim 11; Page 94; 125pp; English.  
XX  
CC The sequence is that of a BS124-specific EST clone.  
CC It is useful for detecting, diagnosing, staging, preventing  
CC or treating, or determining predisposition to diseases or  
CC conditions of the breast, such as breast cancer.  
XX  
SQ Sequence 245 BP; 62 A; 54 C; 89 G; 40 T; 0 other;  
Query Match 100.0%; Score 245; DB 20; Length 245;  
Best Local Similarity 100.0%; Pred. No. 5.2e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 CAGGAGGCCAGGAGGAGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
DB 61 CAGGAGGCCAGGAGGAGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
QY 121 AGCCAGCTTACCTTCATGAGGAGGAGTGTGATCCAGAGAAATTCGTATCGCGAA 180  
DB 121 AGCCAGCTTACCTTCATGAGGAGGAGTGTGATCCAGAGAAATTCGTATCGCGAA 180  
QY 181 GAGGAGGAGGAGTGTGCAATACAGGCGCTATGGGCGAGGAGCTCATGTACCTCAGGA 240  
DB 181 GAGGAGGAGGAGTGTGCAATACAGGCGCTATGGGCGAGGAGCTCATGTACCTCAGGA 240  
QY 241 GCTGC 245  
DB 241 GCTGC 245  
RESULT 2  
AA19505  
ID AA19505 standard; DNA; 522 BP.  
XX  
AC AA19505;  
XX  
DT 07-JUN-1999 (first entry)  
XX  
DE Human lipocalin homologue zlipol encoding DNA SEQ ID NO:1.  
XX  
KW Human; lipocalin; testis; mammary gland; breast tumour; zlipol;  
KW breast cancer; emphysema; skin disease; reproduction; anti-inflammatory;  
KW antimicrobial; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 7..519 /\*tag= a  
XX  
DN W09907740-A2.  
XX  
PD 18-FEB-1999.  
XX  
PF 06-AUG-1998; 98W0-US16425.  
XX  
PR 06-AUG-1997; 97US-0054867.  
XX  
PA (ZYMO) ZYMOGENETICS INC.  
XX  
PI Conklin DC;  
XX  
DR WPI; 1999-167367/14.  
DR P-PSDB; AAW99669.  
XX  
PT New lipocalin homologue designated zlipol - whose expression is

PT restricted to testis and mammary gland tissues, particularly breast  
PT tumour tissue, used to, e.g. predict tumour aggressiveness  
XX  
PS Claim 3; Page 82-83; 94pp; English.  
XX  
CC The present sequence encodes a human lipocalin homologue, designated  
CC zlipol. The lipocalin homologue, zlipol, is specifically expressed in  
CC testis and mammary gland, particularly breast tumour tissue. Based on  
CC this tissue distribution, zlipol may be used as a diagnostic for breast  
CC carcinomas and as a tool for predicting tumour aggressiveness. Agonists  
CC can be used for transportation of small hydrophobic molecules either in  
CC vivo or in vitro, and so are useful in specifically promoting the growth  
CC and/or development of testis-specific cell lineages in culture. Zlipol  
CC can be used to identify inhibitors. Zlipol proteins can also be used to  
CC prepare antibodies (which can be linked to toxins), and can serve as  
CC immunogens. Zlipol proteins can be used as a delivery and encapsulation  
CC system to transport and/or stabilise small lipophilic molecules e.g. to  
CC protect from gut pH and digestive enzymes. They can also be used to bind  
CC small fatty acids in blood or tissues to modulate their biological  
CC function, e.g. to transport retinoids or steroids to receptors, in  
CC particular as therapy for breast cancer, emphysema and diseases of the  
CC skin. They may also play an important role in reproduction. Other uses  
CC include anti-inflammatory responses, and antimicrobial activities.  
CC Zlipol nucleic acid sequences may be used for gene therapy to increase  
CC or inhibit zlipol activity, to derive probes and primers, to derive  
CC antisense sequences, and to detect genetic abnormalities.  
XX  
SQ Sequence 522 BP; 125 A; 132 C; 172 G; 93 T; 0 other;  
Query Match 100.0%; Score 245; DB 20; Length 522;  
Best Local Similarity 100.0%; Pred. No. 6.3e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAGGCCATGCTGATGAGGACCTTCGCGAGGA 60  
DB 75 GGATATCACAGGACCTGGTACGTGAGGCCATGCTGATGAGGACCTTCGCGAGGA 134  
QY 61 CAGGAGGCCAGGAGGAGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
DB 135 CAGGAGGCCAGGAGGAGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 194  
QY 121 AGCCAGCTTACCTTCATGAGGAGGAGTGTGATCCAGAGAAATTCGTATCGCGAA 180  
DB 195 AGCCAGCTTACCTTCATGAGGAGGAGTGTGATCCAGAGAAATTCGTATCGCGAA 254  
QY 181 GAGGAGGAGGAGTGTGCAATACAGGCGCTATGGGCGAGGAGCTCATGTACCTCAGGA 240  
DB 255 GAGGAGGAGGAGTGTGCAATACAGGCGCTATGGGCGAGGAGCTCATGTACCTCAGGA 314  
QY 241 GCTGC 245  
DB 315 GCTGC 319  
RESULT 3  
AAD35179  
ID AAD35179 standard; DNA; 523 BP.  
XX  
AC AAD35179;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Human zlipol DNA.  
XX  
KW Human; lipocalin protein; zlipol; glycodeilin; pheromone; anxiety;  
KW beneficial mood; hypothalamic; satiety; identification; energy balance;  
KW reproductive biology; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 8..517 /\*tag= a

us-09-099-823-2.rng

Mon Feb 10 11:11:44 2003

FT /product= "Human Zlipo1 protein"  
PT /note= "CDS does not include stop codon"  
XX /partial  
PN  
XX WO200223201-A2.  
XX  
XX  
XX PD 21-MAR-2002.  
XX  
XX PF 12-SEP-2001; 2001WO-US28525.  
XX PR 13-SEP-2000; 2000US-232218P.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX  
XX PI Lok S, Foster DC, Holloway JL;  
XX WPI; 2002-362374/39.  
XX P-PSDB; AAE22099.  
XX  
XX PT Use of Zlipo1 or glycode1in (human pheromone polypeptides) for  
PT identifying presence of Zlipo1 receptor, glycode1in receptor, Zlipo1  
PT ligand or glycode1in ligand in test sample  
XX  
XX PS Disclosure; Page 46-47; 50pp; English.  
XX  
XX The invention relates to a method of using two human lipocalin proteins,  
CC Zlipo1 and glycode1in as pheromone polypeptides. Human pheromones are used  
CC to alleviate anxiety, promote beneficial moods and to alter hypothalamic  
CC functions, such as satiety, energy balance and reproductive biology. The  
CC sequences of the invention are used for identifying the presence of  
CC Zlipo1 receptor or a glycode1in receptor in a test sample, or for  
CC identifying the presence of a Zlipo1 ligand or a glycode1in ligand in a  
CC test sample. The present sequence is human Zlipo1 DNA.  
XX  
SQ Sequence 523 BP; 125 A; 133 C; 172 G; 93 T; 0 other;  
Best Local Similarity 100.0%; Score 245; DB 24; Length 523;  
Best Local Similarity 100.0%; Pred. No. 6.4e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATATACACAGGACCTGTACGTGAGGCGCATGTGTGATAGGACTTTCCGGAGGA 60  
DB 76 GATATACACAGGACCTGTGTACGTGAGGCGCATGTGTGATAGGACTTTCCGGAGGA 135  
QY 61 CAGGAGGCCAGGAGGTGTCCTCCAGTGTGAGTGACAGCCCTGGCGGTGGAGTTGGA 120  
DB 136 CAGGAGGCCAGGAGGTGTCCTCCAGTGTGAGTGACAGCCCTGGCGGTGGAGTTGGA 195  
QY 121 AGCCAGCTTCACTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGCGAA 180  
DB 196 AGCCAGCTTCACTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGCGAA 255  
QY 181 GACGAGAGGAGCTTGGCAATACAGCGCTATGCGGCGAGAGAGCTCATGTATCGCGAGGA 240  
DB 256 GACGAGAGGAGCTTGGCAATACAGCGCTATGCGGCGAGAGAGCTCATGTATCGCGAGGA 315  
QY 241 GCTGC 245  
DB 316 GCTGC 320  
RESULT 4  
AAS76054  
ID AAS76054 standard; cDNA; 603 BP.  
XX  
XX AAS76054;  
XX  
XX 13-FEB-2002 (first entry)  
XX  
XX DNA encoding novel human diagnostic protein #11859.  
XX  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.  
OS  
XX WO200175067-A2.  
PN  
XX 11-OCT-2001.  
PD  
XX 30-MAR-2001; 2001WO-US08631.  
PF  
XX 31-MAR-2000; 2000US-0540217.  
PR  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSFQ INC.  
PA  
XX Dmanac RF, Liu C, Tang YT;  
PI  
XX WPI; 2001-639362/73.  
DR  
XX P-PSDB; ABG11867.  
DR  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
XX Claim 1; SEQ ID No 11859; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (I) is useful for generating antibodies against it, detecting or  
CC quantifying a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pet\_sequences.  
XX  
SQ Sequence 603 BP; 142 A; 178 C; 182 G; 101 T; 0 other;  
Query Match 100.0%; Score 245; DB 23; Length 603;  
Best Local Similarity 100.0%; Pred. No. 6.6e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATATACACAGGACCTGTACGTGAGGCGCATGTGTGATAGGACTTTCCGGAGGA 60  
DB 69 GATATACACAGGACCTGTGTGATAGGCGCATGTGTGATAGGACTTTCCGGAGGA 128  
QY 61 CAGGAGGCCAGGAGGTGTCCTCCAGTGTGAGTGACAGCCCTGGCGGTGGAGTTGGA 120  
DB 129 CAGGAGGCCAGGAGGTGTCCTCCAGTGTGAGTGACAGCCCTGGCGGTGGAGTTGGA 188  
QY 121 AGCCAGCTTCACTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGCGAA 180  
DB 189 AGCCAGCTTCACTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGCGAA 248  
QY 181 GACGAGAGGAGCTTGGCAATACAGCGCTATGCGGCGAGAGAGCTCATGTATCGCGAGGA 240  
DB 249 GACGAGAGGAGCTTGGCAATACAGCGCTATGCGGCGAGAGAGCTCATGTATCGCGAGGA 308  
QY 241 GCTGC 245  
DB 309 GCTGC 313

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| ID AAF80043 standard; cDNA; 676 BP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| XX AAF80043;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DT 11-JUN-2001 (first entry)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| DE Nucleotide sequence of odorant binding polypeptide OBP1IB-alpha.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| KW Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| KW anticancer; foetus detoxification; pregnancy marker; ss.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| OS Homo sapiens.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| XX Key Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| FH CDS 43..555                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| FT /*tag= a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| FT /product= "odorant binding polypeptide OBP1IB-alpha"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| PN W0200112806-A2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| PD 22-FEB-2001.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| PF 11-AUG-2000; 200OWO-FR02319.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| PR 13-AUG-1999; 99FR-0010439.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| PA (YUAE-) UNIV AUVERGNE.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| PA (PITI/) PITIOT G.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| PI Pitiot G, Lacazette E, Gachon F;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| DR WPI: 2001-202864/20.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| XX P-PSDB; AAB67742.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| XX New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| XX Disclosure; Page 113-114; 132pp; French.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| XX The present sequence encodes a human odorant binding polypeptide (OBP), designated OBP1B-alpha. OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds for treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foeto-placental pathology (rupture of the amniotic membrane); and as anti-allergic agents. |
| XX Sequence 676 BP; 160 A; 200 C; 204 G; 112 T; 0 other;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| SQ Query Match 100.0%; Score 245; DB 22; Length 676;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Best Local Similarity 100.0%; Pred. No. 6.8e-59;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| OY 1 GGATATCAGGGACCTGTGACTGAAGCCCATCGTGCATGAAGCACTTCGCGAGGA 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 111 GGATATCAGGGACCTGTGACTGAAGCCCATCGTGCATGAAGCACTTCGCGAGGA 170                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

|          |                                                                           |                                                            |     |
|----------|---------------------------------------------------------------------------|------------------------------------------------------------|-----|
| QY       | 61                                                                        | CAGGAGCCGACGAGGTCCTCCACTGTAGGTGACGAGCCTGGCGTGGAGATTGGA     | 120 |
| Db       | 171                                                                       | CRGAGGCCGACGAGAGGTGTCCCGTGAAGTGTGACAGCCCTGGCGTGGAGATTGGA   | 230 |
| QY       | 121                                                                       | AGCCAGCTTCACCTTCATCGAGGGAGATCGGTGATCCAGAGAAATCCTGATGCCGAA  | 180 |
| Db       | 231                                                                       | AGCCAGCTTCACCTTCATCGAGGGAGATCGGTGATCCAGAGAAATCCTGATGCCGAA  | 290 |
| QY       | 181                                                                       | GACGAGGAGCGCTGGCAATACAGCCCTATGTTGGGGGAGAGCTCATGTACCTGCAGGA | 240 |
| Db       | 291                                                                       | GACGAGGAGCGCTGGCAATACAGCCCTATGTTGGGGGAGAGCTCATGTACCTGCAGGA | 350 |
| QY       | 241                                                                       | GCTGC 245                                                  |     |
| Db       | 351                                                                       | GCTGC 355                                                  |     |
| RESULT   | 6                                                                         |                                                            |     |
| AAZ91770 |                                                                           |                                                            |     |
| ID       | AAZ91770                                                                  | standard; DNA; 690 BP.                                     |     |
| AC       | AAZ91770;                                                                 |                                                            |     |
| CD       |                                                                           |                                                            |     |
| DT       | 01-JUN-2000                                                               | (first entry)                                              |     |
| DE       | Human breast specific gene IS clone 1213903.                              |                                                            |     |
| KW       | Human; breast specific gene; breast specific marker; BSG; diagnosis;      |                                                            |     |
| KW       | breast cancer; therapy; SS.                                               |                                                            |     |
| OS       | Homo sapiens.                                                             |                                                            |     |
| PN       | WO2000008210-Al.                                                          |                                                            |     |
| PD       | 17-FEB-2000.                                                              |                                                            |     |
| PF       | 22-JUL-1999; 99WO-US16811.                                                |                                                            |     |
| PR       | 04-AUG-1998; 98US-0095232.                                                |                                                            |     |
| PA       | (DIAD-) DIADEXUS LLC.                                                     |                                                            |     |
| PI       | Sun Y, Recipon H, Cafferkey R;                                            |                                                            |     |
| PS       | WPI; 2000-205737/18.                                                      |                                                            |     |
| PT       | Detecting, diagnosing, monitoring, staging, prognosticating, imaging      |                                                            |     |
| PT       | and treating breast cancer using protein product of breast specific       |                                                            |     |
| PT       | genes -                                                                   |                                                            |     |
| PS       | Example 1; Page 43; 45pp; English.                                        |                                                            |     |
| CC       | This sequence represents a breast specific gene (BSG) clone. The BSG      |                                                            |     |
| CC       | sequences are also referred to as breast specific markers (BSM). The      |                                                            |     |
| CC       | invention relates to methods for diagnosing, monitoring, staging, imaging |                                                            |     |
| CC       | and treating breast cancer (BC). The methods comprise measuring the       |                                                            |     |
| CC       | levels of BSG products in cells, tissues or body fluids of the patient    |                                                            |     |
| CC       | and comparing the measured levels of BSG with BSG levels of a normal      |                                                            |     |
| CC       | human control. An antibody against the BSG sequences can be labelled and  |                                                            |     |
| CC       | used for imaging BC in a patient. The antibody can be conjugated to a     |                                                            |     |
| CC       | cytotoxic agent, and used for treating BC in a patient.                   |                                                            |     |
| XX       | Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;                     |                                                            |     |
| XX       | Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;                     |                                                            |     |

|                       | Query Match    | 100.0%                                                     | Score 245 | DB 21  | Length 690 |
|-----------------------|----------------|------------------------------------------------------------|-----------|--------|------------|
| Best Local Similarity | 100.0%         |                                                            |           |        |            |
| Matches 245           | Conservative 0 | Mismatches 0                                               | Indels 0  | Gaps 0 |            |
| QY                    | 1              | GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGGTGCATAGGNCNCTCCCGGAGA | 60        |        |            |
| Db                    | 113            | GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGGTGCATAGGACCTCCCGGAGA  | 172       |        |            |



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QY 61 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120
DB 173 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232
QY 121 AGCCACGTTCACTTCATGAGGAGGATCGGTGCATCCAGAAAGAAATCTGATCGGAA 180
DB 233 AGCCACGTTCACTTCATGAGGAGGATCGGTGCATCCAGAAAGAAATCTGATCGGAA 292
QY 181 GACGAGGAGCCCTGGCAAAATACAGCCCTATGGGGCAGGAAGCTCATGTGACGAGGA 240
DB 293 GACGAGGAGCCCTGGCAAAATACAGCCCTATGGGGCAGGAAGCTCATGTGACGAGGA 352
QY 241 GCTGC 245
DB 353 GCTGC 357

RESULT 7
AA07456
ID AAX07456 standard; cDNA; 692 BP.
XX
AC AAX07456;
XX
DT 08-JUN-1999 (first entry)
XX
DE Human BS124 specific EST clone 1730294IH.
XX
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;
XX EST; ss.
XX
OS Homo sapiens.
XX
PN WO9859049-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US12862.
XX
PR 20-JUN-1997; 97US-0879354.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billig-medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Russell JC, Scheffel CP, Stroupe SD, Yu H;
XX
DR WPI; 1999-105623/09.
XX
PT New isolated BS124 polynucleotides and polypeptides - used for
PT detecting, diagnosing, preventing or treating diseases or conditions
PT of the breast, such as breast cancer
XX
PS Claim 11; Pages 94-95; 125pp; English.
XX
CC The sequence is that of a BS124-specific EST clone.
CC It is useful for detecting, diagnosing, staging, preventing
CC or treating, or determining predisposition to diseases or
CC conditions of the breast, such as breast cancer.
XX
SQ Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;

Query Match 100.0%; Score 245; DB 20; Length 692;
Best Local Similarity 100.0%; Pred. No. 6.8e-59;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGTGATGAGGCCATGGTGTGATGATGAGGACTTTCGGAGGA 60
DB 113 GGATATCACAGGACCTGTGATGAGGCCATGGTGTGATGATGAGGACTTTCGGAGGA 172
QY 61 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120
DB 173 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232
QY 61 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120
DB 173 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232
QY 61 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120
DB 173 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232

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QY 121 AGCCACGTTCACTTCATGAGGAGGATCGGTGCATCCAGAAAGAAATCTGATCGGAA 180
DB 233 AGCCACGTTCACTTCATGAGGAGGATCGGTGCATCCAGAAAGAAATCTGATCGGAA 292
QY 181 GACGAGGAGCCCTGGCAAAATACAGCCCTATGGGGCAGGAAGCTCATGTGACGAGGA 240
DB 293 GACGAGGAGCCCTGGCAAAATACAGCCCTATGGGGCAGGAAGCTCATGTGACGAGGA 352
QY 241 GCTGC 245
DB 353 GCTGC 357

RESULT 8
AA07457
ID AAX07457 standard; cDNA; 692 BP.
XX
AC AAX07457;
XX
DT 08-JUN-1999 (first entry)
XX
DE Human BS124 specific EST clone consensus sequence.
XX
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;
XX consensus; EST; ss.
XX
OS Homo sapiens.
XX
PN WO9859049-A1.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-US12862.
XX
PR 20-JUN-1997; 97US-0879354.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billig-medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Russell JC, Scheffel CP, Stroupe SD, Yu H;
XX
DR WPI; 1999-105623/09.
XX
PT New isolated BS124 polynucleotides and polypeptides - used for
PT detecting, diagnosing, preventing or treating diseases or conditions
PT of the breast, such as breast cancer
XX
PS Claim 11; Page 95; 125pp; English.
XX
CC The sequence is that of a consensus BS124-specific EST clone.
CC It is useful for detecting, diagnosing, staging, preventing
CC or treating, or determining predisposition to diseases or
CC conditions of the breast, such as breast cancer.
XX
SQ Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;

Query Match 100.0%; Score 245; DB 20; Length 692;
Best Local Similarity 100.0%; Pred. No. 6.8e-59;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGTGATGAGGCCATGGTGTGATGATGAGGACTTTCGGAGGA 60
DB 113 GGATATCACAGGACCTGTGATGAGGCCATGGTGTGATGATGAGGACTTTCGGAGGA 172
QY 61 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120
DB 173 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232
QY 121 AGCCACGTTCACTTCATGAGGAGGATCGGTGCATCCAGAAAGAAATCTGATCGGAA 180
DB 233 AGCCACGTTCACTTCATGAGGAGGATCGGTGCATCCAGAAAGAAATCTGATCGGAA 292

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QY 181 GAGGAGGAGCCTGGCAATACAGGCTTATGGGGCAGGAAGCTCATGTACCTGCAGGA 240  
 DB 293 GAGGAGGAGCCTGGCAATACAGGCTTATGGGGCAGGAAGCTCATGTACCTGCAGGA 352  
 QY 241 GCTGC 245  
 DB 353 GCTGC 357  
 RESULT 9  
 AAF54313 standard; DNA; 738 BP.  
 AC AAF54313;  
 XX AAF54313;  
 DT 02-APR-2001 (first entry)  
 XX DNA encoding protein of the invention #50.  
 XX Secreted; transmembrane; gene therapy; ss.  
 XX Unidentified.  
 XX WO200078961-A1.  
 PN 28-DEC-2000.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 29-OCT-1999; 99US-0162506.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 02-DEC-1999; 99WO-US28551.  
 XX 16-DEC-1999; 99WO-US30095.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 06-JAN-2000; 2000WO-US00376.  
 PA (GETH) GENENTECH INC.  
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski EJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
 PI Watanabe CK, Williams PM, Wood WI;  
 DR WPI; 2001-071395/08.  
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy -  
 XX  
 PS Claim 2; Fig 99; 787pp; English.  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of  
 CC anti-sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents.  
 CC The nucleic acids may also be used in gene therapy.  
 XX  
 SQ Sequence 738 BP; 209 A; 207 C; 205 G; 117 T; 0 other;  
 Query Match 100.0%; Score 245; DB 22; Length 738;  
 Best Local Similarity 100.0%; Pred No. 6.9e-59;  
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGATATCACAGGAGCCTGGTACCTGAGGCGCATGTGGTGTGATAGAGCTTCGCGAGGA 60  
 DB 113 GGATATCACAGGAGCCTGGTACCTGAGGCGCATGTGGTGTGATAGAGCTTCGCGAGGA 172

QY 61 CAGGAGGCCAGGAAGGTGCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
 DB 173 CAGGAGGCCAGGAAGGTGCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232  
 QY 121 AGCCACGTTCCATCTTCATGAGGAGGATCGGTGCATCCAGAGAAATCCTGATGCGGAA 180  
 DB 233 AGCCACGTTCCATCTTCATGAGGAGGATCGGTGCATCCAGAGAAATCCTGATGCGGAA 292  
 QY 181 GACGGAGAGCCTGGCAATACAGGCTTATGGGGCAGGAAGCTCATGTACCTGCAGGA 240  
 DB 293 GACGGAGAGCCTGGCAATACAGGCTTATGGGGCAGGAAGCTCATGTACCTGCAGGA 352  
 QY 241 GCTGC 245  
 DB 353 GCTGC 357  
 RESULT 10  
 AAC58615 standard; cDNA; 739 BP.  
 ID AAC58615  
 XX AAC58615;  
 AC AAC58615;  
 DT 29-JAN-2001 (first entry)  
 XX Human PRO1283 protein UNQ653 encoding cDNA SEQ ID NO:169.  
 DE Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
 KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; thyroiditis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; diabetes mellitus;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053758-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 02-MAR-2000; 2000WO-US05841.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123577.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20344.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 16-DEC-1999; 99WO-US28565.  
PR 20-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US30999.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PA (GETH) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;  
XX WPI; 2000-572271/53.  
DR P-PDS; AAB33450.  
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
XX Claim 23; Fig 73; 309pp; English.  
XX The present invention describes sixty four human PRO proteins which can  
CC be used in the treatment of immune related diseases. The human PRO  
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
CC treating and diagnosing immune related disorders. The disorders are  
CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinating diseases of the central  
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
CC autoimmune or immune-mediated skin diseases, allergic diseases,  
CC immunological diseases of the lung, and transplantation associated  
CC diseases including graft rejection and graft-versus-host-disease.  
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;  
SQ

Query Match 100.0%; Score 245; DB 21; Length 739;  
Best Local Similarity 100.0%; Fred. No. 7e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGNATACACGAGGACCTGGTACGTAGAGCCATGCTGCTGATAGAGACTTCCGAGGA 60  
Db 113 GGNATACACGAGGACCTGGTACGTAGAGCCATGCTGCTGATAGAGACTTCCGAGGA 172  
Qy 61 CAGGAGGCCAGGAGGTGTCCCTAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
Db 173 CAGGAGGCCAGGAGGTGTCCCTAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232  
Qy 121 AGCCACGTTTCACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGGAA 180  
Db 233 AGCCACGTTTCACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGGAA 292  
Qy 181 CAGCGAGGAGCTGGCAATACAGCCCTATGGGGGCGAGAGACCTCATGACCTCGGAA 240  
Db 293 CAGCGAGGAGCTGGCAATACAGCCCTATGGGGGCGAGAGACCTCATGACCTCGGAA 352

QY 241 GCTGC 245  
Db 353 GCTGC 357  
RESULT 11  
AAA37071  
ID AAA37071 standard; cDNA; 739 BP.  
XX AC AAA37071;  
XX DT 08-AUG-2000 (first entry)  
XX DE Human PRO1283 (UNG653) cDNA sequence SEQ ID NO:161.  
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening;  
XX ss.  
XX OS Homo sapiens.  
XX PN WO200012708-A2.  
XX PD 09-MAR-2000.  
XX PF 01-SEP-1999; 99WO-US20111.  
XX PR 01-SEP-1998; 98US-0098716.  
XX PR 01-SEP-1998; 98US-0098749.  
XX PR 02-SEP-1998; 98US-0098803.  
XX PR 02-SEP-1998; 98US-0098821.  
XX PR 02-SEP-1998; 98US-0098843.  
XX PR 02-SEP-1998; 98US-0098936.  
XX PR 02-SEP-1998; 98US-0098956.  
XX PR 02-SEP-1998; 98US-0098958.  
XX PR 02-SEP-1998; 98US-0098962.  
XX PR 02-SEP-1998; 98US-0098964.  
XX PR 10-SEP-1998; 98US-0099741.  
XX PR 10-SEP-1998; 98US-0099754.  
XX PR 10-SEP-1998; 98US-0099763.  
XX PR 10-SEP-1998; 98US-0099792.  
XX PR 10-SEP-1998; 98US-0099808.  
XX PR 10-SEP-1998; 98US-0099812.  
XX PR 10-SEP-1998; 98US-0099815.  
XX PR 10-SEP-1998; 98US-0099816.  
XX PR 15-SEP-1998; 98US-0100385.  
XX PR 15-SEP-1998; 98US-0100388.  
XX PR 15-SEP-1998; 98US-0100390.  
XX PR 16-SEP-1998; 98US-0100584.  
XX PR 16-SEP-1998; 98US-0100627.  
XX PR 16-SEP-1998; 98US-0100661.  
XX PR 16-SEP-1998; 98US-0100662.  
XX PR 16-SEP-1998; 98US-0100664.  
XX PR 17-SEP-1998; 98US-0100683.  
XX PR 17-SEP-1998; 98US-0100710.  
XX PR 17-SEP-1998; 98US-0100711.  
XX PR 17-SEP-1998; 98US-0100919.  
XX PR 17-SEP-1998; 98US-0100930.  
XX PR 18-SEP-1998; 98US-0100848.  
XX PR 18-SEP-1998; 98US-0100849.  
XX PR 18-SEP-1998; 98US-0101014.  
XX PR 18-SEP-1998; 98US-0101068.  
XX PR 18-SEP-1998; 98US-0101071.  
XX PR 22-SEP-1998; 98US-0101279.  
XX PR 23-SEP-1998; 98US-0101471.  
XX PR 23-SEP-1998; 98US-0101472.  
XX PR 23-SEP-1998; 98US-0101474.  
XX PR 23-SEP-1998; 98US-0101475.  
XX PR 23-SEP-1998; 98US-0101476.  
XX PR 23-SEP-1998; 98US-0101477.

PR 23-SEP-1998; 98US-0101479.  
PR 24-SEP-1998; 98US-0101738.  
PR 24-SEP-1998; 98US-0101741.  
PR 24-SEP-1998; 98US-0101743.  
PR 24-SEP-1998; 98US-0101915.  
PR 24-SEP-1998; 98US-0101916.  
PR 29-SEP-1998; 98US-0102207.  
PR 29-SEP-1998; 98US-0102240.  
PR 29-SEP-1998; 98US-0102307.  
PR 29-SEP-1998; 98US-0102330.  
PR 29-SEP-1998; 98US-0102331.  
PR 30-SEP-1998; 98US-0102484.  
PR 30-SEP-1998; 98US-0102487.  
PR 30-SEP-1998; 98US-0102570.  
PR 30-SEP-1998; 98US-0102571.  
PR 01-OCT-1998; 98US-0102684.  
PR 01-OCT-1998; 98US-0102687.  
PR 02-OCT-1998; 98US-0102965.  
PR 06-OCT-1998; 98US-0103258.  
PR 06-OCT-1998; 98US-0103449.  
PR 07-OCT-1998; 98US-0103314.  
PR 07-OCT-1998; 98US-0103315.  
PR 07-OCT-1998; 98US-0103328.  
PR 07-OCT-1998; 98US-0103395.  
PR 07-OCT-1998; 98US-0103396.  
PR 07-OCT-1998; 98US-0103401.  
PR 08-OCT-1998; 98US-0103633.  
PR 08-OCT-1998; 98US-0103678.  
PR 08-OCT-1998; 98US-0103679.  
PR 08-OCT-1998; 98US-0103711.  
PR 14-OCT-1998; 98US-0104257.  
PR 20-OCT-1998; 98US-0104987.  
PR 20-OCT-1998; 98US-0105000.  
PR 20-OCT-1998; 98US-0105002.  
PR 21-OCT-1998; 98US-0105104.  
PR 22-OCT-1998; 98US-0105169.  
PR 22-OCT-1998; 98US-0105266.  
PR 26-OCT-1998; 98US-0105693.  
PR 26-OCT-1998; 98US-0105694.  
PR 27-OCT-1998; 98US-0105807.  
PR 27-OCT-1998; 98US-0105881.  
PR 27-OCT-1998; 98US-0105882.  
PR 28-OCT-1998; 98US-0106062.  
PR 28-OCT-1998; 98US-0106023.  
PR 28-OCT-1998; 98US-0106029.  
PR 28-OCT-1998; 98US-0106030.  
PR 28-OCT-1998; 98US-0106032.  
PR 28-OCT-1998; 98US-0106033.  
PR 28-OCT-1998; 98US-0106178.  
PR 29-OCT-1998; 98US-0106248.  
PR 29-OCT-1998; 98US-0106384.  
PR 29-OCT-1998; 98US-0108500.  
PR 30-OCT-1998; 98US-0106464.  
PR 03-NOV-1998; 98US-0106856.  
PR 03-NOV-1998; 98US-0106902.  
PR 03-NOV-1998; 98US-0106905.  
PR 03-NOV-1998; 98US-0106919.  
PR 03-NOV-1998; 98US-0106932.  
PR 03-NOV-1998; 98US-0106934.  
PR 10-NOV-1998; 98US-0107783.  
PR 17-NOV-1998; 98US-0108775.  
PR 17-NOV-1998; 98US-0108779.  
PR 17-NOV-1998; 98US-0108787.  
PR 17-NOV-1998; 98US-0108788.  
PR 17-NOV-1998; 98US-0108801.  
PR 17-NOV-1998; 98US-0108802.  
PR 17-NOV-1998; 98US-0108806.  
PR 17-NOV-1998; 98US-0108807.  
PR 17-NOV-1998; 98US-0108867.  
PR 17-NOV-1998; 98US-0108925.  
PR 18-NOV-1998; 98US-0108848.  
PR 18-NOV-1998; 98US-0108849.  
PR 18-NOV-1998; 98US-0108850.

PR 18-NOV-1998; 98US-0108851.  
PR 18-NOV-1998; 98US-0108852.  
PR 18-NOV-1998; 98US-0108858.  
PR 18-NOV-1998; 98US-0108904.  
XX (GETH ) GENENTECH INC.  
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CX, Wood WL;  
XX WPI; 2000-237871/20.  
DR P-PSDB; AA193389.  
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of Potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions  
XX Claim 2; Fig 99; 773pp; English.  
XX AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AA99340 to AA99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding them have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.  
XX Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;  
SQ Query Match 100.0%; Score 245; DB 21; Length 739;  
Best Local Similarity 100.0%; Pred. No. 7e-59; 0; Indels 0; Gaps 0;  
Matches 245; Conservative 0; Mismatches 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGCTGTCGATGAGACTTTCCGGAGGA 60  
DB 113 GGATATCACAGGACCTGGTACGTGAAGGCCATGCTGTCGATGAGACTTTCCGGAGGA 172  
QY 61 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
DB 173 CAGGAGGCCAGGAAGGTGTCCCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 232  
QY 121 AGCCACGTTCCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCTGATCGCGAA 180  
DB 233 AGCCACGTTCCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCTGATCGCGAA 292  
QY 181 GACGAGGAGCCCTGCAATACAGGCGCTATGGGGCAGGAGCTCATGTACTCGAGGA 240  
DB 293 GACGAGGAGCCCTGCAATACAGGCGCTATGGGGCAGGAGCTCATGTACTCGAGGA 352  
QY 241 GCTGC 245  
DB 353 GCTGC 357  
RESULT 12  
ABL95663  
ID ABL95663 standard; cDNA; 739 BP.  
XX ABL95663;  
XX 19-JUL-2002 (first entry)  
XX Human angiogenesis related cDNA PRO1283 SEQ ID NO: 205.  
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
XX cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
XX antiarteriosclerotic; gene; ss.  
XX Homo sapiens.  
XX WO200208284-A2.  
PN

XX PD 31-JAN-2002.  
XX PF 09-JUL-2001; 2001WO-US21735.  
XX PR 20-JUL-2000; 2000US-219556P.  
XX PR 25-JUL-2000; 2000US-220624P.  
XX PR 25-JUL-2000; 2000US-220664P.  
XX PR 28-JUL-2000; 2000WO-US20710.  
XX PR 02-AUG-2000; 2000US-222695P.  
XX PR 17-AUG-2000; 2000US-0643657.  
XX PR 23-AUG-2000; 2000WO-US23328.  
XX PR 24-AUG-2000; 2000WO-US23328.  
XX PR 07-SEP-2000; 2000US-230978P.  
XX PR 15-SEP-2000; 2000US-000000P.  
XX PR 18-SEP-2000; 2000US-0664610.  
XX PR 18-SEP-2000; 2000US-0665350.  
XX PR 24-OCT-2000; 2000US-242922P.  
XX PR 08-NOV-2000; 2000US-0709238.  
XX PR 10-NOV-2000; 2000WO-US30952.  
XX PR 01-DEC-2000; 2000WO-US30873.  
XX PR 01-DEC-2000; 2000WO-US32678.  
XX PR 20-DEC-2000; 2000US-0747259.  
XX PR 22-DEC-2000; 2000WO-US34956.  
XX PR 22-JAN-2001; 2001US-0767609.  
XX PR 28-FEB-2001; 2001US-0796498.  
XX PR 01-MAR-2001; 2001WO-US06520.  
XX PR 09-MAR-2001; 2001US-0802706.  
XX PR 14-MAR-2001; 2001US-0808689.  
XX PR 22-MAR-2001; 2001US-0816744.  
XX PR 05-APR-2001; 2001US-0828366.  
XX PR 10-MAY-2001; 2001US-0854208.  
XX PR 10-MAY-2001; 2001US-0854280.  
XX PR 25-MAY-2001; 2001US-0866028.  
XX PR 25-MAY-2001; 2001US-0866034.  
XX PR 25-MAY-2001; 2001WO-US17092.  
XX PR 30-MAY-2001; 2001US-0870574.  
XX PR 01-JUN-2001; 2001WO-US17443.  
XX PR 20-JUN-2001; 2001WO-US17800.  
XX PR 28-JUN-2001; 2001WO-US00000.

XX PA (GETH ) GENENTECH INC.  
XX PA (BAKE/) BAKER K P.  
XX PA (FERR/) FERRARA N.  
XX PA (GERB/) GERBER H.  
XX PA (GERR/) GERRITSEN M E.  
XX PA (GODD/) GODDARD A.  
XX PA (GODO/) GODOWSKI P J.  
XX PA (GURN/) GURNEY A L.  
XX PA (HILL/) HILLAN K J.  
XX PA (MARS/) MARSTERS S A.  
XX PA (PANJ/) PAN J.  
XX PA (PAON/) PAONI N F.  
XX PA (STEP/) STEPHAN J F.  
XX PA (WATA/) WATANABE C K.  
XX PA (WILL/) WILLIAMS P M.  
XX PA (WOOD/) WOOD W I.

XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NF;  
XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
XX PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX DR WPI; 2002-171999/22.  
XX DR P-PSDB; ABB95525.

XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX PT infarction), endothelial or angiogenic disorders in a mammal  
XX PS Claim 1; Fig 205; 567pp; English.

CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.  
XX SQ Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;

Query Match 100.0%; Score 245; DB 24; Length 739;  
Best Local Similarity 100.0%; Pred. No. 7e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGTACGTGAAGCCATGTGTGTGATAGGACTTTCCGAGGA 60  
DB 113 GGATATCACAGGACCTGTACGTGAAGCCATGTGTGTGATAGGACTTTCCGAGGA 172  
QY 61 CAGGAGCCCGCAGGAGGTGTCACAGTGAAGGTGACAGCCCTGGCGGTGGAGTTTGA 120  
DB 173 CAGGAGCCCGCAGGAGGTGTCACAGTGAAGGTGACAGCCCTGGCGGTGGAGTTTGA 232  
QY 121 AGCCAGCTTCACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCTGATCGGAA 180  
DB 233 AGCCAGCTTCACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCTGATCGGAA 292  
QY 181 GACGAGGAGCCTTGGCAAAATACAGCCCTATGGGGCAGGAACTCTATGTCGAGGA 240  
DB 293 GACGAGGAGCCTTGGCAAAATACAGCCCTATGGGGCAGGAACTCTATGTCGAGGA 352  
QY 241 GCTGC 245  
DB 353 GCTGC 357

RESULT 13  
ABL86174  
ID ABL86174 standard; cDNA; 739 BP.  
XX AC ABL86174;  
XX DT 16-MAY-2002 (first entry)  
XX DE Human PRO1283 cDNA sequence SEQ ID NO:205.

XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
XX KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX KW age-related macular degeneration; arterial restenosis; angina;  
XX KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX KW wound healing; chromosome mapping; gene mapping; gene; ss.

XX OS Homo sapiens.  
XX PR WO200200690-A2.  
XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US19692.  
XX PR 23-JUN-2000; 2000US-213637P.  
XX PR 20-JUL-2000; 2000US-219556P.  
XX PR 25-JUL-2000; 2000US-220624P.  
XX PR 25-JUL-2000; 2000US-220664P.  
XX PR 28-JUL-2000; 2000WO-US20710.  
XX PR 02-AUG-2000; 2000US-222695P.  
XX PR 17-AUG-2000; 2000US-0643657.  
XX PR 23-AUG-2000; 2000WO-US23328.  
XX PR 24-AUG-2000; 2000WO-US23328.  
XX PR 07-SEP-2000; 2000US-230978P.



Query Match 98.0%; Score 240.2; DB 22; Length 676;  
Best Local Similarity 98.8%; Pred. No. 1.5e-57;  
Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGTTACCTGAAGCCATGTTGTCGATTAAGGACTTCCGGAGGA 60  
DB 111 GGATATCACAGGACCTGTTACCTGAAGCCATGTTGTCGATTAAGGACTTCCGGAGGA 170  
QY 61 CAGGAGGCCAGGAGGTGTCCTCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
DB 171 CAGGAGGCCAGGAGGTGTCCTCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 230  
QY 121 AGCCAGCTTACCTTCATCAGGAGGATCGGTGCTATCCGAGAAATCTGATCGGAA 180  
DB 231 AGCCAGCTTACCTTCATCAGGAGGATCGGTGCTATCCGAGAAATCTGATCGGAA 290  
QY 181 GACGAGGAGGAGCCTGGCAAAATACAGCCCTATGGGGGCGAGGAGCTCATGTACTCGAGGA 240  
DB 291 GACGAGGAGGAGCCTGGCAAAATACAGCCCTATGGGGGCGAGGAGCTCATGTACTCGAGGA 350  
QY 241 GCTGC 245  
DB 351 GCTGC 355

RESULT 15  
AAFP80040  
ID AAFP80040 standard; cDNA; 725 BP.  
AC AAFP80040;  
XX AAFP80040;  
DI 11-JUN-2001 (first entry)  
DE Nucleotide sequence of odorant binding polypeptide OBPIIa-beta.  
KW Odorant binding polypeptide; OBPII; hydrophobic ligand; odorant; allergy;  
KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;  
KW anticancer; foetus detoxification; pregnancy marker; ss.  
XX Homo sapiens.

Key Location/Qualifiers  
FH 43..483  
FT /\*tag= a  
FT /product= "odorant binding polypeptide OBPIIa-beta"  
XX WC200112806-A2.  
XX 22-FEB-2001.  
XX 11-AUG-2000; 2000WO-FR02319.  
XX 12-AUG-1999; 99FR-0010439.  
XX (UYAU-) UNIV AUVERGNE.  
XX (PITI/) PITOT G.  
XX Pitot G, Lacazette E, Gachon F;  
XX WPI; 2001-202864/20.  
XX P-PSDB; AAB67739.

New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes  
PS Claim 6; Page 108-109; 132pp; French.  
XX The present sequence encodes a human odorant binding polypeptide (OBPII), designated OBPIIa-beta. OBPIIs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc... OBPII polypeptides are used as binding proteins for

CC hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBPII, also in analysis of complex perfume mixtures; or to supplement non-maternal for treating hyperlipidemia or obesity; or to supplement food additives; as a milk when combined with nutritional fatty acids; as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foeto-placental pathology (rupture of the amniotic membrane); and as CC antiallergic agents.  
XX  
SQ Sequence 725 BP; 163 A; 222 C; 217 G; 123 T; 0 other;

Query Match 98.0%; Score 240.2; DB 22; Length 725;  
Best Local Similarity 98.8%; Pred. No. 1.5e-57;  
Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGTTACCTGAAGCCATGTTGTCGATTAAGGACTTCCGGAGGA 60  
DB 111 GGATATCACAGGACCTGTTACCTGAAGCCATGTTGTCGATTAAGGACTTCCGGAGGA 170  
QY 61 CAGGAGGCCAGGAGGTGTCCTCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
DB 171 CAGGAGGCCAGGAGGTGTCCTCAAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 230  
QY 121 AGCCAGCTTACCTTCATCAGGAGGATCGGTGCTATCCGAGAAATCTGATCGGAA 180  
DB 231 AGCCAGCTTACCTTCATCAGGAGGATCGGTGCTATCCGAGAAATCTGATCGGAA 290  
QY 181 GACGAGGAGGAGCCTGGCAAAATACAGCCCTATGGGGGCGAGGAGCTCATGTACTCGAGGA 240  
DB 291 GACGAGGAGGAGCCTGGCAAAATACAGCCCTATGGGGGCGAGGAGCTCATGTACTCGAGGA 350  
QY 241 GCTGC 245  
DB 351 GCTGC 355

Search completed: February 9, 2003, 22:02:10  
Job time : 94.0132 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 20:30:25 ; Search time 17.8084 Seconds  
(without alignments)  
4219.129 Million cell updates/sec

Title: US-09-099-823-2  
Perfect score: 245  
Sequence: 1 GGATATCAGAGGACCTGGT.....CATGTACTGAGAGCTGC 245

Scoring table: IDENTITY\_NTC  
Gap 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description       |
|------------|-------|-------|--------|-------|-------------------|
| 1          | 245   | 100.0 | 522    | 3     | US-09-130-663-1   |
| 2          | 245   | 100.0 | 522    | 3     | US-09-432-335-1   |
| 3          | 245   | 100.0 | 522    | 4     | US-09-614-022-1   |
| 4          | 181   | 73.9  | 510    | 3     | US-09-130-663-5   |
| 5          | 181   | 73.9  | 510    | 3     | US-09-432-335-5   |
| 6          | 181   | 73.9  | 510    | 4     | US-09-614-022-5   |
| 7          | 70.4  | 28.7  | 525    | 2     | US-08-467-603-1   |
| 8          | 70.4  | 28.7  | 525    | 2     | US-08-466-793-1   |
| 9          | 70.4  | 28.7  | 525    | 2     | US-08-491-861A-1  |
| 10         | 52    | 21.2  | 147    | 3     | US-09-130-663-16  |
| 11         | 52    | 21.2  | 147    | 3     | US-09-130-663-24  |
| 12         | 52    | 21.2  | 147    | 3     | US-09-432-335-16  |
| 13         | 52    | 21.2  | 147    | 3     | US-09-432-335-24  |
| 14         | 52    | 21.2  | 147    | 4     | US-09-614-022-16  |
| 15         | 52    | 21.2  | 147    | 4     | US-09-614-022-24  |
| 16         | 46    | 18.8  | 52     | 3     | US-09-130-663-15  |
| 17         | 46    | 18.8  | 52     | 3     | US-09-432-335-15  |
| 18         | 46    | 18.8  | 52     | 4     | US-09-614-022-15  |
| 19         | 40    | 16.3  | 7218   | 1     | US-08-232-463-14  |
| 20         | 39.2  | 16.0  | 2338   | 1     | US-08-425-069-1   |
| 21         | 39.2  | 16.0  | 2338   | 2     | US-08-317-844B-1  |
| 22         | 38.8  | 15.8  | 289    | 4     | US-09-007-005-17  |
| 23         | 38.8  | 15.8  | 289    | 4     | US-09-244-796-17  |
| 24         | 34.4  | 14.0  | 1872   | 1     | US-08-153-848-39  |
| 25         | 34.4  | 14.0  | 1872   | 3     | US-09-299-843A-39 |
| 26         | 34.4  | 14.0  | 1872   | 4     | US-09-088-337B-39 |
| 27         | 34.4  | 14.0  | 1872   | 5     | PCT-US93-11153-39 |

|    |      |      |       |   |                   |
|----|------|------|-------|---|-------------------|
| 28 | 34.2 | 14.0 | 3979  | 4 | US-09-085-199B-10 |
| 29 | 33.6 | 13.7 | 1368  | 4 | US-09-237-357-98  |
| 30 | 33.6 | 13.7 | 2456  | 3 | US-08-813-150-5   |
| 31 | 33   | 13.5 | 867   | 3 | US-08-869-696-6   |
| 32 | 33   | 13.5 | 1044  | 3 | US-08-869-696-20  |
| 33 | 33   | 13.5 | 1282  | 3 | US-08-869-696-21  |
| 34 | 33   | 13.5 | 1372  | 3 | US-08-869-696-22  |
| 35 | 33   | 13.5 | 1690  | 3 | US-08-869-696-8   |
| 36 | 33   | 13.5 | 3435  | 1 | US-08-366-577-1   |
| 37 | 33   | 13.5 | 3435  | 5 | PCT-US96-00005-1  |
| 38 | 33   | 13.5 | 5529  | 3 | US-08-869-696-1   |
| 39 | 32.8 | 13.4 | 243   | 1 | US-08-182-175A-56 |
| 40 | 32.8 | 13.4 | 243   | 1 | US-08-474-633A-74 |
| 41 | 32.8 | 13.4 | 243   | 4 | US-08-823-771-74  |
| 42 | 32.8 | 13.4 | 243   | 5 | PCT-US92-06412-56 |
| 43 | 32.8 | 13.4 | 15872 | 4 | US-09-105-537-1   |
| 44 | 32   | 13.1 | 2522  | 3 | US-09-062-416-13  |
| 45 | 31.6 | 12.9 | 5515  | 4 | US-09-398-193-98  |

ALIGNMENTS

RESULT 1  
US-09-130-663-1  
; Sequence 1, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)...(516)  
US-09-130-663-1

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|-----------------------|--------|-----------------------------------------------------------|-------|-------------|
| Query Match           | 100.0% | Score 245;                                                | DB 3; | Length 522; |
| Best Local Similarity | 100.0% | Pred. No. 4.5e-59;                                        |       |             |
| Matches               | 245;   | Conservative                                              | 0;    | Mismatches  |
| Indels                | 0;     | Gaps                                                      | 0;    |             |
| QY                    | 1      | GGATATCAGAGGACCTGGTACTGAGGCGCATGTGTGTCGATAGGACTTTTCGGAGGA | 60    |             |
| Db                    | 75     | GGATATCAGAGGACCTGGTACTGAGGCGCATGTGTGTCGATAGGACTTTTCGGAGGA | 134   |             |
| QY                    | 61     | CAGGAGGCCAGGAGGTGTCGCCAGTGAAGTGCACAGCCCTGGCGGTGGGAAGTTGGA | 120   |             |
| Db                    | 135    | CAGGAGGCCAGGAGGTGTCGCCAGTGAAGTGCACAGCCCTGGCGGTGGGAAGTTGGA | 194   |             |
| QY                    | 121    | AGCCACGTTTCACCTTCATGAGGAGGATTCGGTGCATCCAGAAATTCCTGATCCGGA | 180   |             |
| Db                    | 195    | AGCCACGTTTCACCTTCATGAGGAGGATTCGGTGCATCCAGAAATTCCTGATCCGGA | 254   |             |
| QY                    | 181    | GACGAGGAGGCTGGCAATACAGAGGCTATGGGGGAGGAGGCTCATGTACCTCAGGA  | 240   |             |
| Db                    | 255    | GACGAGGAGGCTGGCAATACAGAGGCTATGGGGGAGGAGGCTCATGTACCTCAGGA  | 314   |             |
| QY                    | 241    | GCTGC                                                     | 245   |             |
| Db                    | 315    | GCTGC                                                     | 319   |             |

RESULT 2  
US-09-432-335-1



; Sequence 1, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; PRIOR APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1999-11-02  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)...(516)  
US-09-432-335-1

Query Match 100.0%; Score 245; DB 3; Length 522;  
Best Local Similarity 100.0%; Pred. No. 4.5e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGTGATGAAGCACTTTCCGGAGGA 60  
Db 75 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGTGATGAAGCACTTTCCGGAGGA 134  
QY 61 CAGGAGCCCGCAGAGAGGTGCCAGTGAAGTGACAGCCCTGGGCGTGGGAAGTTGA 120  
Db 135 CAGGAGCCCGCAGAGAGGTGCCAGTGAAGTGACAGCCCTGGGCGTGGGAAGTTGA 194  
QY 121 AGCCAGCTTCACCTTCATGAGGAGGATCGTGATCCAGAGAAATCTGATCGGAA 180  
Db 135 CAGGAGCCCGCAGAGAGGTGCCAGTGAAGTGACAGCCCTGGGCGTGGGAAGTTGA 194  
QY 195 AGCCAGCTTCACCTTCATGAGGAGGATCGTGATCCAGAGAAATCTGATCGGAA 254  
Db 195 AGCCAGCTTCACCTTCATGAGGAGGATCGTGATCCAGAGAAATCTGATCGGAA 254  
QY 181 GACGAGGAGCCCTGGCAATACAGCGCTATGGGGCGAGGAAGCTCATGTACCTGCAGGA 240  
Db 255 GACGAGGAGCCCTGGCAATACAGCGCTATGGGGCGAGGAAGCTCATGTACCTGCAGGA 314  
QY 241 GCTGC 245  
Db 315 GCTGC 319

RESULT 3  
US-09-614-022-1  
; Sequence 1, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; PRIOR APPLICATION NUMBER: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)...(516)  
US-09-614-022-1

Query Match 100.0%; Score 245; DB 4; Length 522;  
Best Local Similarity 100.0%; Pred. No. 4.5e-59;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGTGATGAAGCACTTTCCGGAGGA 60  
Db 75 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGTGATGAAGCACTTTCCGGAGGA 134  
QY 61 CAGGAGCCCGCAGAGAGGTGCCAGTGAAGTGACAGCCCTGGGCGTGGGAAGTTGA 120  
Db 135 CAGGAGCCCGCAGAGAGGTGCCAGTGAAGTGACAGCCCTGGGCGTGGGAAGTTGA 194  
QY 121 AGCCAGCTTCACCTTCATGAGGAGGATCGTGATCCAGAGAAATCTGATCGGAA 180  
Db 195 AGCCAGCTTCACCTTCATGAGGAGGATCGTGATCCAGAGAAATCTGATCGGAA 254  
QY 181 GACGAGGAGCCCTGGCAATACAGCGCTATGGGGCGAGGAAGCTCATGTACCTGCAGGA 240  
Db 255 GACGAGGAGCCCTGGCAATACAGCGCTATGGGGCGAGGAAGCTCATGTACCTGCAGGA 314  
QY 241 GCTGC 245  
Db 315 GCTGC 319  
RESULT 4  
US-09-130-663-5  
; Sequence 5, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 510  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate sequence derived from human zipol  
; OTHER INFORMATION: nucleotide sequence  
; NAME/KEY: variation  
; LOCATION: (1)...(510)  
; OTHER INFORMATION: n is any nucleotide  
US-09-130-663-5

Query Match 73.9%; Score 181; DB 3; Length 510;  
Best Local Similarity 61.6%; Pred. No. 2.2e-41;  
Matches 151; Conservative 52; Mismatches 42; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGTGATGAAGCACTTTCCGGAGGA 60  
Db 69 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGTGATGAAGCACTTTCCGGAGGA 128  
QY 61 CAGGAGCCCGCAGAGAGGTGCCAGTGAAGTGACAGCCCTGGGCGTGGGAAGTTGA 120  
Db 129 YGNGNCCNNGNNAAGTNNNSCCNNGTNAAGTNNNSCCNNGTNNNSCCNNGTNNNS 188  
QY 121 AGCCAGCTTCACCTTCATGAGGAGGATCGTGATCCAGAGAAATCTGATCGGAA 180  
Db 189 RGCNACNTTACNTTATGNGAGAGTNGTGTATCAARARARATHTYNTNGMNA 248  
QY 181 GACGAGGAGCCCTGGCAATACAGCGCTATGGGGCGAGGAAGCTCATGTACCTGCAGGA 240  
Db 249 RACNGAGCAGCCNNGNNAAGTNNNSCCNNGTNNNSCCNNGTNNNSCCNNGTNNNS 308  
QY 241 GCTGC 245

Db 309 RYTC 313

RESULT 5  
US-09-432-335-5  
; Sequence 5, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; EARLIER FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 510  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate sequence derived from human zlipol  
; NAME/KEY: variation  
; LOCATION: (1)...(510)  
; OTHER INFORMATION: n is any nucleotide  
US-09-432-335-5

Query Match 73.9%; Score 181; DB 3; Length 510;  
Best Local Similarity 61.6%; Pred. No. 2.2e-41;  
Matches 151; Conservative 52; Mismatches 42; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGCTACGTGAGGCGCTGGTGGTGCATGAGGACTTCCGGAGGA 60  
DB 69 RGATATCACAGGACCTGCTACGTGAGGCGCTGGTGGTGCATGAGGACTTCCGGAGGA 128  
QY 61 CAGGAGGCCAGAGAGGTGCCCGAGTGAAGTGCACAGCCCTGGCGGTGGGAAGTTGA 120  
DB 129 YMGNGCCMGNAAGTGNACGCTGATGAGGAGGAGTGTGATGAGGAGGAGGAGGAGG 188  
QY 121 AGCCAGCTTCCATGATGAGGAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGG 180  
DB 189 RCGNACNTTYACNTTYATGAGGAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGG 248  
QY 181 GAGGAGGAGGCTGGCAATACAGCCCTATGGGCGAGGAGGAGGAGGAGGAGGAGG 240  
DB 249 RACNGAGAGCCGNGNAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 308  
QY 241 GCTGC 245  
DB 309 RYTC 313

RESULT 6  
US-09-614-022-5  
; Sequence 5, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; EARLIER FILING DATE: 2000-07-11  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 510  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate sequence derived from human zlipol  
; NAME/KEY: variation  
; LOCATION: (1)...(510)  
; OTHER INFORMATION: n is any nucleotide  
US-09-614-022-5  
Query Match 73.9%; Score 181; DB 4; Length 510;  
Best Local Similarity 61.6%; Pred. No. 2.2e-41;  
Matches 151; Conservative 52; Mismatches 42; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGCTACGTGAGGCGCTGGTGGTGCATGAGGACTTCCGGAGGA 60  
DB 69 RGATATCACAGGACCTGCTACGTGAGGCGCTGGTGGTGCATGAGGACTTCCGGAGGA 128  
QY 61 CAGGAGGCCAGAGAGGTGCCCGAGTGAAGTGCACAGCCCTGGCGGTGGGAAGTTGA 120  
DB 129 YMGNGCCMGNAAGTGNACGCTGATGAGGAGGAGTGTGATGAGGAGGAGGAGGAGG 188  
QY 121 AGCCAGCTTCCATGATGAGGAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGG 180  
DB 189 RCGNACNTTYACNTTYATGAGGAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGG 248  
QY 181 GAGGAGGAGGCTGGCAATACAGCCCTATGGGCGAGGAGGAGGAGGAGGAGGAGG 240  
DB 249 RACNGAGAGCCGNGNAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 308  
QY 241 GCTGC 245  
DB 309 RYTC 313

RESULT 7  
US-08-467-603-1  
; Sequence 1, Application US/08467603  
; Patent No. 5843672  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanieczny, Andrey  
; APPLICANT: Bizindakas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and  
; TITLE OF INVENTION: Peptides from Dog  
; TITLE OF INVENTION: Bander and Uses Therefor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,603  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/156,549  
; FILING DATE:  
; APPLICATION NUMBER: 07/999,712  
; FILING DATE: 31-Dec-92  
; ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 1..525  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 79..525  
US-08-467-603-1

Query Match 28.7%; Score 70.4; DB 2; Length 525;  
Best Local Similarity 59.2%; Pred. No. 7.9e-11;  
Matches 141; Conservative 0; Mismatches 91; Indels 6; Gaps 1;  
QY 1 GGATATCAGAGGACCTGGTACGTGAGAGGCCATGCTGCTGATAGAGGACTTCCGAGGA 60  
DB 87 GCGTGTCTCAGGGAATGGTATCTGAGAGGCCATGACAGACAGGAGGTGCTGA--- 143  
QY 61 CAGGAGGCCAGGAGGTGCTCCCGAGGTGAGGTGACAGCCCTGGCGGTGGAGGTGGA 120  
DB 144 ---GAAGCTGACTCAGTGACTCCCGAGGTGAGGTGACAGCCCGAGGAGGTGGA 200  
QY 121 AGCCAGTTCACCTCTCAGGAGGAGTCCGTCATCCAGAGAAATCTGTATCGGAA 180  
DB 201 AGCCAGATCACCCTGTCGAATGTCAGTCCGACAGACATCCGCGGTGCTGCACAA 260  
QY 181 GACGAGGAGCTGGCAATATACAGCCCTATGCGGAGGAGGAGTCTATGATCTGAG 238  
DB 261 AACCTTGAGCCTGGCAATATACAGCCATACAGAGGCCAGCGGTGCTGATCCAG 318

RESULT 8  
US-08-466-793-1  
Sequence 1, Application US/08466793  
Patent No. 5891716  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrey  
APPLICANT: Bizindauskas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and  
TITLE OF INVENTION: Peptides from Dog  
TITLE OF INVENTION: Dander and Uses Therefor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,793  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156,549

FILING DATE: 22-NOV-1993  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 1..525  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 79..525  
US-08-466-793-1  
Query Match 28.7%; Score 70.4; DB 2; Length 525;  
Best Local Similarity 59.2%; Pred. No. 7.9e-11;  
Matches 141; Conservative 0; Mismatches 91; Indels 6; Gaps 1;  
QY 1 GGATATCAGAGGACCTGGTACGTGAGAGGCCATGCTGCTGATAGAGGACTTCCGAGGA 60  
DB 87 GCGTGTCTCAGGGAATGGTATCTGAGAGGCCATGACAGACAGGAGGTGCTGA--- 143  
QY 61 CAGGAGGCCAGGAGGTGCTCCCGAGGTGAGGTGACAGCCCTGGCGGTGGAGGTGGA 120  
DB 144 ---GAAGCTGACTCAGTGACTCCCGAGGTGAGGTGACAGCCCGAGGAGGTGGA 200  
QY 121 AGCCAGTTCACCTCTCAGGAGGAGTCCGTCATCCAGAGAAATCTGTATCGGAA 180  
DB 201 AGCCAGATCACCCTGTCGAATGTCAGTCCGACAGACATCCGCGGTGCTGCACAA 260  
QY 181 GACGAGGAGCTGGCAATATACAGCCCTATGCGGAGGAGGAGTCTATGATCTGAG 238  
DB 261 AACCTTGAGCCTGGCAATATACAGCCATACAGAGGCCAGCGGTGCTGATCCAG 318

RESULT 9  
US-08-491-861A-1  
Sequence 1, Application US/08491861A  
Patent No. 5939283  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrey  
APPLICANT: Bizindauskas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
TITLE OF INVENTION: Dander and Uses Therefor  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,861A  
FILING DATE: 27-OCT-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-0266CP (IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..525  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 79..525  
US-08-491-861A-1

Query Match 28.7%; Score 70.4; DB 2; Length 525;

Best Local Similarity 59.2%; Pred. No. 7.9e-11;  
Matches 141; Conservative 0; Mismatches 91; Indels 6; Gaps 1;

QY 1 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTTTCGAGGA 60  
DB 87 GCGTGTGTCAGGGAATGCTATCTGAAGCCATGACAGCAGGAGGTGCTGA--- 143  
QY 61 CAGGAGGCGCAGGAGGCTCTCCCGATGAGGTGACAGCCCTGGCGGTGGA 120  
DB 144 ---GAGCCTGACTGCTGCTCCATGCTCTCAAGCCAGAGGGGGGCACTGGA 200  
QY 121 ACCGATGTCACCTCAGCAGGAGGATCGGTGATCCAGAGAAATCTGATCGGAA 180  
DB 201 ACCGATGTCACCTCAGCAGGAGGATCGGTGATCCAGAGAAATCTGATCGGAA 260  
QY 181 GAGCAGGAGGCTGCGCAATACAGCCCTATGCGGCGCAGGAGCTCATGTACCTCCAG 238  
DB 261 AACCTGAGCCTGCGCAATACAGCCCTATGCGGCGCAGGAGCTCATGTACCTCCAG 318

RESULT 10  
US-09-130-663-16  
; Sequence 16, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: NEP-tagged linker  
US-09-130-663-16

Query Match 21.2%; Score 52; DB 3; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTT 52  
DB 96 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTT 147

## RESULT 11

US-09-130-663-24  
; Sequence 24, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Flag linker  
US-09-130-663-24

Query Match 21.2%; Score 52; DB 3; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTT 52  
DB 96 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTT 147

## RESULT 12

US-09-432-335-16  
; Sequence 16, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; EARLIER FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: NEE-tagged linker  
US-09-432-335-16

Query Match 21.2%; Score 52; DB 3; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTT 52  
DB 96 GGATATCACAGGACCTGCTAGCTGAAGCCATGCTGTGCGATGAAGACTT 147

## RESULT 13

US-09-432-335-24  
; Sequence 24, Application US/09432335  
; Patent No. 6143720

GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; CURRENT FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Flag linker  
US-09-432-335-24

Query Match 21.2%; Score 52; DB 3; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGGTCGATAGGACTTT 52  
|||||  
Db 96 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGGTCGATAGGACTTT 147

## RESULT 14

US-09-614-022-16  
; Sequence 16, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/054,867  
; PRIOR FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: NEE-tagged linker  
US-09-614-022-16

Query Match 21.2%; Score 52; DB 4; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGGTCGATAGGACTTT 52  
|||||  
Db 96 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGGTCGATAGGACTTT 147

## RESULT 15

US-09-614-022-24  
; Sequence 24, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663

US-09-614-022-24  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/054,867  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Flag linker  
US-09-614-022-24  
Query Match 21.2%; Score 52; DB 4; Length 147;  
Best Local Similarity 100.0%; Pred. No. 6.8e-06;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGGTCGATAGGACTTT 52  
|||||  
Db 96 GGATATCACAGGACCTGGTACGTGAAGCCATGGTGGTCGATAGGACTTT 147  
Search completed: February 9, 2003, 22:05:05  
Job time : 21.8084 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 21:14:50 ; Search time 18.8877 Seconds  
(without alignments)  
6148.496 Million cell updates/sec

Title: US-09-099-823-2  
Perfect score: 245  
Sequence: 1 GGATACACAGGACCTGGT.....CATGTACCTGCAGGAGCTGC 245

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA.\*

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Query No. | Score | Match | Length | DB ID               | Description       |
|------------|-----------|-------|-------|--------|---------------------|-------------------|
| 1          | 245       | 100.0 | 245   | 10     | US-09-099-823-2     | Sequence 2, Appl  |
| 2          | 245       | 100.0 | 523   | 10     | US-09-951-845-1     | Sequence 1, Appl  |
| 3          | 245       | 100.0 | 692   | 10     | US-09-099-823-4     | Sequence 4, Appl  |
| 4          | 245       | 100.0 | 692   | 10     | US-09-099-823-5     | Sequence 5, Appl  |
| 5          | 185       | 75.5  | 336   | 10     | US-09-833-381-1747  | Sequence 1747, Ap |
| 6          | 150.6     | 61.5  | 501   | 10     | US-09-833-381-803   | Sequence 803, App |
| 7          | 124       | 50.6  | 236   | 10     | US-09-099-823-1     | Sequence 1, Appl  |
| 8          | 70.4      | 28.7  | 525   | 10     | US-09-374-671-1     | Sequence 11281, A |
| 9          | 38.2      | 15.6  | 264   | 10     | US-09-878-574-11281 | Sequence 11281, A |
| 10         | 38.2      | 15.6  | 299   | 10     | US-09-878-574-11878 | Sequence 59, Appl |
| 11         | 38.2      | 15.6  | 285   | 10     | US-09-878-574-59    | Sequence 2305, Ap |
| 12         | 38.2      | 15.6  | 391   | 10     | US-09-878-574-2305  | Sequence 1, Appl  |
| 13         | 36        | 14.7  | 1464  | 9      | US-10-166-359-1     | Sequence 1, Appl  |
| 14         | 36        | 14.7  | 1464  | 9      | US-10-166-113-1     | Sequence 1, Appl  |
| 15         | 36        | 14.7  | 1464  | 9      | US-10-166-357-1     | Sequence 1, Appl  |
| 16         | 36        | 14.7  | 1464  | 9      | US-10-166-372-1     | Sequence 1, Appl  |
| 17         | 36        | 14.7  | 1464  | 10     | US-09-149-045-1     | Sequence 1, Appl  |
| 18         | 35.2      | 14.4  | 882   | 10     | US-09-947-744-3     | Sequence 3, Appl  |
| 19         | 35        | 14.3  | 1852  | 10     | US-09-969-852-4     | Sequence 4, Appl  |

|    |      |      |       |    |                     |                    |
|----|------|------|-------|----|---------------------|--------------------|
| 20 | 34.6 | 14.1 | 381   | 10 | US-09-878-574-3730  | Sequence 3730, Ap  |
| 21 | 34.2 | 14.0 | 1934  | 10 | US-09-815-242-7960  | Sequence 7960, Ap  |
| 22 | 33.6 | 13.7 | 1368  | 9  | US-09-983-802-98    | Sequence 98, Appl  |
| 23 | 33.6 | 13.7 | 1982  | 10 | US-09-813-358-217   | Sequence 217, Appl |
| 24 | 33.2 | 13.6 | 804   | 9  | US-09-949-449-3     | Sequence 3, Appl   |
| 25 | 32.8 | 13.4 | 1098  | 10 | US-09-815-242-7874  | Sequence 7874, Ap  |
| 26 | 32.8 | 13.4 | 1680  | 9  | US-09-364-847-20    | Sequence 20, Appl  |
| 27 | 32.8 | 13.4 | 2571  | 9  | US-09-364-847-32    | Sequence 32, Appl  |
| 28 | 32.8 | 13.4 | 2571  | 9  | US-09-364-847-34    | Sequence 34, Appl  |
| 29 | 32.8 | 13.4 | 15872 | 9  | US-09-860-846-1     | Sequence 1, Appl   |
| 30 | 32.8 | 13.4 | 32189 | 10 | US-09-861-289-1     | Sequence 1, Appl   |
| 31 | 32.8 | 13.4 | 32189 | 10 | US-09-764-878-379   | Sequence 379, App  |
| 32 | 32.8 | 13.4 | 32221 | 10 | US-09-764-878-377   | Sequence 377, App  |
| 33 | 32.2 | 13.1 | 382   | 10 | US-09-960-352-5442  | Sequence 5442, App |
| 34 | 32.2 | 13.1 | 447   | 9  | US-09-796-692-8254  | Sequence 8254, App |
| 35 | 32.2 | 13.1 | 948   | 10 | US-09-886-055-194   | Sequence 194, App  |
| 36 | 32.2 | 13.1 | 2519  | 10 | US-09-969-708-281   | Sequence 281, App  |
| 37 | 32.2 | 13.1 | 2519  | 10 | US-09-880-107-2189  | Sequence 2189, App |
| 38 | 32   | 13.1 | 144   | 10 | US-09-864-761-27403 | Sequence 27403, A  |
| 39 | 32   | 13.1 | 450   | 10 | US-09-867-550-1671  | Sequence 1671, A   |
| 40 | 32   | 13.1 | 493   | 10 | US-09-864-761-10761 | Sequence 10761, A  |
| 41 | 32   | 13.1 | 714   | 9  | US-10-015-219-1204  | Sequence 1204, Ap  |
| 42 | 32   | 13.1 | 714   | 9  | US-09-777-564-1204  | Sequence 1204, Ap  |
| 43 | 32   | 13.1 | 2602  | 10 | US-09-917-800A-1590 | Sequence 1590, Ap  |
| 44 | 32   | 13.1 | 5515  | 10 | US-09-751-100B-98   | Sequence 98, Appl  |
| 45 | 31.6 | 12.9 |       |    |                     |                    |

## ALIGNMENTS

RESULT 1  
US-09-099-823-2  
Sequence 2, Application US/09099823  
Patent No. US20020016990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099, 823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-099-823-2

Query Match 100.0%; Score 245; DB 10; Length 245;  
Best Local Similarity 100.0%; Pred. No. 8.2e-61;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGCGATAGAGACTTCCGGAGGA 60  
DB 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGCGATAGAGACTTCCGGAGGA 60  
QY 61 CAGGAGGCCAGGAAGGTGTCCCGAGTGAAGTGCAGAGCCCTGGCGTGGGAAGTTGGA 120  
DB 61 CAGGAGGCCAGGAAGGTGTCCCGAGTGAAGTGCAGAGCCCTGGCGTGGGAAGTTGGA 120  
QY 121 AGCCAGGTTACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGGAA 180  
DB 121 AGCCAGGTTACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGGAA 180  
QY 181 GAGGAGGAGCTGCGAATATACGCCCTTATGGGCGCAGGAGCTCATGTACTCGAGGA 240  
DB 181 GAGGAGGAGCTGCGAATATACGCCCTTATGGGCGCAGGAGCTCATGTACTCGAGGA 240  
QY 241 GCTGC 245  
DB 241 GCTGC 245

RESULT 2  
US-09-951-845-1  
Sequence 1, Application US/09951845  
Patent No. US20020098497A1  
GENERAL INFORMATION:  
APPLICANT: LOK, Si  
APPLICANT: Foster, Donald C.  
APPLICANT: Holloway, James L.  
TITLE OF INVENTION: Use of Human Pheromone Polypeptides  
FILE REFERENCE: 00-85  
CURRENT APPLICATION NUMBER: US/09/951,845  
CURRENT FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 523  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (8)...(517)  
US-09-951-845-1

Query Match 100.0%; Score 245; DB 10; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1e-60;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGCGATAGAGACTTCCGGAGGA 60  
DB 76 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGCGATAGAGACTTCCGGAGGA 135  
QY 61 CAGGAGGCCAGGAAGGTGTCCCGAGTGAAGTGCAGAGCCCTGGCGTGGGAAGTTGGA 120  
DB 135 CAGGAGGCCAGGAAGGTGTCCCGAGTGAAGTGCAGAGCCCTGGCGTGGGAAGTTGGA 195

QY 121 AGCCAGGTTACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGGAA 180  
DB 196 AGCCAGGTTACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATCGGAA 255  
QY 181 GAGGAGGAGCTGCGAATATACGCCCTTATGGGCGCAGGAGCTCATGTACTCGAGGA 240  
DB 256 GAGGAGGAGCTGCGAATATACGCCCTTATGGGCGCAGGAGCTCATGTACTCGAGGA 315  
QY 241 GCTGC 245  
DB 316 GCTGC 320

RESULT 3  
US-09-099-823-4  
Sequence 4, Application US/0909823  
Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 692 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-099-823-4

Query Match 100.0%; Score 245; DB 10; Length 692;  
Best Local Similarity 100.0%; Pred. No. 1.1e-60;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGATGAAGACTTTCCGGAGGA 60  
DB 113 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGATGAAGACTTTCCGGAGGA 172  
QY 61 CAGGAGCCCGCAGAGAGGTGCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGA 120  
DB 173 CAGGAGCCCGCAGAGAGGTGCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGA 232  
QY 121 AGCCACGTTCCCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCATGCGGAA 180  
DB 233 AGCCACGTTCCCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCATGCGGAA 292  
QY 181 GACGAGGAGCCTGGCAAAATACAGCGCCTATGCGGCGAGGAAGTCTCATGCTGCGAA 240  
DB 293 GACGAGGAGCCTGGCAAAATACAGCGCCTATGCGGCGAGGAAGTCTCATGCTGCGAA 352  
QY 241 GCTGC 245  
DB 353 GCTGC 357

RESULT 4

US-09-099-823-5  
; Sequence 5, Application US/09099823  
; Patent No. US2002018990A1  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRANADOS, EDWARD M.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: SCHEFFEL, CHRISTI  
; APPLICANT: STROUPE, STEPHEN D.  
; APPLICANT: YU, HONG  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/099,823  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/879,354  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6120.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/938-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 692 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-099-823-5  
Query Match 100.0%; Score 245; DB 10; Length 692;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06; Indels 0; Gaps 0;  
Matches 245; Conservative 0; Mismatches 0;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGATGAAGACTTTCCGGAGGA 60  
DB 113 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGATGAAGACTTTCCGGAGGA 172  
QY 61 CAGGAGCCCGCAGAGAGGTGCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGA 120  
DB 173 CAGGAGCCCGCAGAGAGGTGCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGA 232  
QY 121 AGCCACGTTCCCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCATGCTGCGAA 180  
DB 233 AGCCACGTTCCCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCATGCTGCGAA 292  
QY 181 GACGAGGAGCCTGGCAAAATACAGCGCCTATGCGGCGAGGAAGTCTCATGCTGCGAA 240  
DB 293 GACGAGGAGCCTGGCAAAATACAGCGCCTATGCGGCGAGGAAGTCTCATGCTGCGAA 352  
QY 241 GCTGC 245  
DB 353 GCTGC 357

RESULT 5

US-09-833-381-1747  
; Sequence 1747, Application US/09833381  
; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: ROBISON, Keith E.  
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 3800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1747  
; LENGTH: 336  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-833-381-1747  
Query Match 75.5%; Score 185; DB 10; Length 336;  
Best Local Similarity 99.0%; Pred. No. 9.8e-44;  
Matches 207; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
QY 1 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGATGAAGACTTTCCGGAGG 59  
DB 128 GGATATCACAGGACCTGGTACGTGAAGGCCATGGTGTGATGAAGACTTTCCGGAGG 187  
QY 60 ACAGAGGCCCGCAGAGAGGTGCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGG 119  
DB 188 ACAGAGGCCCGCAGAGAGGTGCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGG 247  
QY 120 AAGCCACGTTCCCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCATGCTGCG 178  
DB 248 AAGCCACGTTCCCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTCATGCTGCG 307  
QY 179 AAGAGCGAGGAGCCTGGCAAAATACAGCGC 207  
DB 308 AAGAGCGAGGAGCCTGGCAAAATACAGCGC 336

RESULT 6

US-09-833-381-803/c





INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..525  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 79..525  
US-09-374-671-1

Query Match 28.7%; Score 70.4; DB 10; Length 525;  
Best Local Similarity 59.2%; Pred. No. 3.8e-11;  
Matches 141; Conservative 0; Mismatches 91; Indels 6; Gaps 1;

QY 1 GGATATCACAGGACCTGTGACGTGAGGCCATGTTGGTGTGATGAAGACTTTCCGGAGGA 60  
DB 87 GGCTGTGTACAGGAATGTATCTGAAGGCCATGACAGCAGCAGGAGGTGCTGTA--- 143  
QY 61 CAGGAGGCCAGGAGGTGTCGCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
DB 144 ---GAGCCTGACTCAGTCACTCCCATGATCTCAAGCCCAAGAGGGGGCAACTTGA 200  
QY 121 AGCCAGGTTCACCTTCATGAGGAGGATCGTGTCTATCCAGAGAAATCTCTGATCGGAA 180  
DB 201 AGCCAGATCACCATCTGCAATGTGTGAGTCCAGAGCATCACGTTGTCTGCAAA 260  
QY 181 CAGGAGAGGCTTGGCAATACAGAGCCCTATGGGGCAGAGCACTCACTGACCTGAC 238  
DB 261 AACTCTGAGCCTGGCAATACAGAGCCATACAGAGGCCACGCTGCTGTTCATCCAG 318

RESULT 9  
US-09-878-574-11281  
; Sequence 11281, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrium, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 11281  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 701064263H1  
US-09-878-574-11281

Query Match 15.6%; Score 38.2; DB 10; Length 264;  
Best Local Similarity 50.8%; Pred. No. 0.045;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 55 GGAGACAGAGGAGCCCGGAGAGAGCCAGTGTCCAGTGAAGGTGACAGCCCTGGCGGTGGAA 114  
DB 82 GCGAGAGAGAGAGCCCGGAGAGAGAGCCAGCGCGGAGAGAGCCCGCGGAGAGAA 141  
QY 115 GTTGGAGAGCCAGTTCACCTTCATGAGGAGGATCGTGTATCCAGAGAAATCTGTAT 174  
DB 142 GCGAGAGGCTTAGAAGAGATCTCGAGAGAGAGGAGGAGGAGGAGAGAGAGAGGAC 201  
QY 175 GCGAGAGAGGAGGAGCCCTGGCAATATACAGCCCTATGGGGCAGGAGTCTATGTACC 233

DB 203 GAAGAAGAGCGTGGAGAGCTTCAAGATCTATCTTCAAGGTCTCTCAGCAGAGTTCACC 261

RESULT 11  
US-09-878-574-59  
; Sequence 59, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrium, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 59  
; LENGTH: 385  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LTB3028-056-Q1-B1-D8  
US-09-878-574-59

Query Match 15.6%; Score 38.2; DB 10; Length 385;  
Best Local Similarity 50.8%; Pred. No. 0.049;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 55 GGAGACAGAGGAGCCCGGAGAGAGCCAGTGTCCAGTGAAGGTGACAGCCCTGGCGGTGGAA 114  
DB 84 GCGAGAGAGAGAGCCCGGAGAGAGAGCCAGTGTCCAGTGAAGGTGACAGCCCGGAGAGAA 143

DB 202 GAAGAAGCGTGGAGACCTACAGATCTATCTTCAAGGTCTCTCAGCAGAGTTCACC 260

RESULT 10  
US-09-878-574-11878  
; Sequence 11878, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrium, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT APPLICATION NUMBER: US/09/878,574  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 11878  
; LENGTH: 299  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 701065017H1  
US-09-878-574-11878

Query Match 15.6%; Score 38.2; DB 10; Length 299;  
Best Local Similarity 50.8%; Pred. No. 0.046;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 55 GCGAGAGAGAGAGCCCGGAGAGAGCCAGTGTCCAGTGAAGGTGACAGCCCTGGCGGTGGAA 114  
DB 83 GCGAGAGAGAGAGCCCGGAGAGAGAGCCAGTGTCCAGTGAAGGTGACAGCCCGGAGAGAA 142  
QY 115 GTTGGAGAGCCAGTTCACCTTCATGAGGAGGATCGTGTATCCAGAGAAATCTGTAT 174  
DB 143 GCGAGAGGCGCCAGAGAGATCTCGAGAGAGGAGGAGGAGGAGAGAGAGAGAGCGAC 202  
QY 175 GCGAGAGAGAGAGAGCCCTGGCAATATACAGCCCTATGGGGCAGGAGTCTATGTACC 233  
DB 203 GAAGAAGAGCGTGGAGAGCTTCAAGATCTATCTTCAAGGTCTCTCAGCAGAGTTCACC 261

QY 115 GTTGAAGCCAGCTTCATCTGATGAGGAGGATCGGTGATCCAGAGAAATCTGAT 174  
DB 144 GCGAGCGGAGAGAGAGATCTGAGGAGGAGGAGGAGAGAGAGAGAGAGG 203  
QY 175 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 233  
DB 204 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 262

## RESULT 12

US-09-878-574-2305

; Sequence 2305, Application US/09878574

; Patent No. US20020110548A1

; GENERAL INFORMATION:

; APPLICANT: BYTUM, Joseph R.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Thompson, Michael D.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(15401)B

; CURRENT APPLICATION NUMBER: US/09/878,574

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/333,535

; NUMBER OF SEQ ID NOS: 15775

; SEQ ID NO 2305

; LENGTH: 391

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: LIB3028-026-01-B1-G3

US-09-878-574-2305

Query Match 15.5%; Score 38.2; DB 10; Length 391;  
Best Local Similarity 50.8%; Pred. No. 0.049;  
Matches 91; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 55 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 114  
DB 83 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142  
QY 115 GTTGAAGCCAGCTTCATCTGATGAGGAGGATCGGTGATCCAGAGAAATCTGAT 174  
DB 143 GCGAGCGGAGAGAGAGATCTGAGGAGGAGGAGGAGGAGAGAGAGAGAGAG 202  
QY 175 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 233  
DB 203 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261

## RESULT 13

US-10-166-359-1/C

; Sequence 1, Application US/10166359

; Publication No. US20030003447A1

; GENERAL INFORMATION:

; APPLICANT: DOMS, ROBERT W.

; APPLICANT: FAULDS, DARYL

; APPLICANT: HESSELGESSER, JOSEPH E.

; APPLICANT: HORUK, RICHARD

; APPLICANT: MITROVIC, BRANISLAVA

; APPLICANT: ZHOU, YIJOING

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING THE INTERACTION

; FILE REFERENCE: BERLX-73(D2)

; CURRENT APPLICATION NUMBER: US/10/166,359

; PRIOR FILING DATE: 2002-08-23

; PRIOR APPLICATION NUMBER: 09/149,045

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1464

; TYPE: DNA

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (199)..(1338)  
US-10-166-359-1

Query Match 14.7%; Score 36; DB 9; Length 1464;  
Best Local Similarity 54.5%; Pred. No. 0.29;  
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 88 GAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAAGCCACGTTACATTCATGAGGAGGA 147  
DB 573 GAAGCTGAGCGCGGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 514  
QY 148 TCGGTGCATCCAGAGAGAAATCTGATGCGGAGAGAGAGAGAGAGAGAGAGAG 207  
DB 513 GCTGAGCTTCGAGAGAGAGGTCCCAAGAGGCCAGTTCATAGTCCCGGTACGTAGGTAGC 454  
QY 208 CTATGGGGGCGAG 219  
DB 453 CCACAGGGGCGAG 442

## RESULT 14

US-10-166-113-1/C

; Sequence 1, Application US/10166113

; Publication No. US20030008279A1

; GENERAL INFORMATION:

; APPLICANT: DOMS, ROBERT W.

; APPLICANT: FAULDS, DARYL

; APPLICANT: HESSELGESSER, JOSEPH E.

; APPLICANT: HORUK, RICHARD

; APPLICANT: MITROVIC, BRANISLAVA

; APPLICANT: ZHOU, YIJOING

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING THE INTERACTION

; FILE REFERENCE: BERLX-73(D3)

; CURRENT APPLICATION NUMBER: US/10/166,113

; PRIOR FILING DATE: 2002-08-23

; PRIOR APPLICATION NUMBER: 09/149,045

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1464

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (199)..(1338)

## RESULT 15

US-10-166-357-1/C

; Sequence 1, Application US/10166357

; Publication No. US20030008379A1



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:05:30 ; Search time 681.035 Seconds  
(without alignments)  
5826.269 Million cell updates/sec

Title: US-09-099-823-2  
Perfect score: 245  
Sequence: 1 GATATCACAGGACCTGGT.....CATGTACTGACGAGGCTGC 245

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- 1: em\_estba:\*\*
- 2: em\_esthum:\*\*
- 3: em\_estlin:\*\*
- 4: em\_estm:\*\*
- 5: em\_estov:\*\*
- 6: em\_estpl:\*\*
- 7: em\_estro:\*\*
- 8: em\_htc:\*\*
- 9: gb\_est1:\*\*
- 10: gb\_est2:\*\*
- 11: gb\_htc:\*\*
- 12: gb\_est3:\*\*
- 13: gb\_est4:\*\*
- 14: gb\_est5:\*\*
- 15: em\_estfun:\*\*
- 16: em\_estom:\*\*
- 17: gb\_gss:\*\*
- 18: em\_gss\_hum:\*\*
- 19: em\_gss\_inv:\*\*
- 20: em\_gss\_pln:\*\*
- 21: em\_gss\_vrt:\*\*
- 22: em\_gss\_fun:\*\*
- 23: em\_gss\_mam:\*\*
- 24: em\_gss\_mus:\*\*
- 25: em\_gss\_other:\*\*
- 26: em\_gss\_pro:\*\*
- 27: em\_gss\_rod:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| c 1        | 168   | 68.6        | 532    | 10 AW513637 | AW513637 x047h10.x |
| c 2        | 145   | 59.2        | 499    | 9 A1219510  | A1219510 qb24d02.x |
| c 3        | 134.8 | 55.0        | 513    | 9 AA977608  | AA977608 cb61e03.s |
| c 4        | 134.4 | 54.9        | 337    | 12 BF193883 | BF193883 245614 YA |
| c 5        | 128.8 | 52.6        | 477    | 9 A1251747  | A1251747 qb90f12.x |
| c 6        | 97.8  | 39.9        | 494    | 14 R47029   | R47029 Y358 Rat In |

RESULT 1  
AW513637/c  
LOCUS

DEFINITION

similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. ; mRNA

ACCESSION

AW513637

VERSION

EST.

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1. (bases 1 to 532)

AUTHORS

NCI-CCAP

TITLE

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cyspb-r@mail.nih.gov

|   |    |      |      |     |    |          |
|---|----|------|------|-----|----|----------|
| c | 7  | 92.2 | 37.5 | 431 | 9  | AA936288 |
|   | 8  | 90.6 | 37.0 | 519 | 9  | A1877463 |
|   | 9  | 90.6 | 37.0 | 603 | 10 | BB618239 |
|   | 10 | 90.6 | 37.0 | 626 | 10 | BB028765 |
|   | 11 | 79.4 | 32.4 | 415 | 9  | AA460385 |
|   | 12 | 70.2 | 28.7 | 594 | 10 | AA320286 |
|   | 13 | 61.6 | 25.1 | 462 | 13 | EM087898 |
|   | 14 | 57   | 23.3 | 438 | 12 | BF603580 |
|   | 15 | 53.4 | 21.8 | 454 | 12 | BF603580 |
|   | 16 | 50.8 | 20.7 | 513 | 12 | BF403550 |
|   | 17 | 43.8 | 17.9 | 224 | 10 | AA316476 |
|   | 18 | 42.4 | 17.3 | 501 | 10 | AA049121 |
|   | 19 | 42.4 | 17.3 | 665 | 14 | BB040745 |
|   | 20 | 42.2 | 17.2 | 584 | 10 | BE517891 |
|   | 21 | 42   | 17.1 | 436 | 10 | AW158517 |
|   | 22 | 42   | 17.1 | 437 | 10 | AW158842 |
|   | 23 | 42   | 17.1 | 518 | 12 | EG814151 |
|   | 24 | 41.8 | 17.1 | 243 | 14 | EQ461186 |
|   | 25 | 41.8 | 17.1 | 339 | 14 | EQ461044 |
|   | 26 | 41.8 | 17.1 | 551 | 14 | EQ469025 |
|   | 27 | 41.8 | 17.1 | 576 | 14 | EQ463781 |
|   | 28 | 41.8 | 17.1 | 647 | 13 | BI954086 |
|   | 29 | 41.8 | 17.1 | 663 | 13 | BI957662 |
|   | 30 | 41.8 | 17.1 | 805 | 12 | BF267509 |
|   | 31 | 41.8 | 17.1 | 820 | 12 | BF265032 |
|   | 32 | 41.8 | 17.1 | 847 | 13 | BI953660 |
|   | 33 | 41.8 | 17.1 | 875 | 12 | BF267309 |
|   | 34 | 41.4 | 16.9 | 356 | 10 | BE481242 |
|   | 35 | 40.4 | 16.5 | 500 | 10 | BE424286 |
|   | 36 | 40.4 | 16.5 | 621 | 10 | AA447921 |
|   | 37 | 40.4 | 16.4 | 621 | 14 | BQ605577 |
|   | 38 | 40.2 | 16.3 | 929 | 12 | BF066082 |
|   | 39 | 40   | 16.3 | 538 | 9  | AL588422 |
|   | 40 | 40   | 16.3 | 581 | 9  | AL588768 |
|   | 41 | 40   | 16.3 | 600 | 12 | BG709987 |
|   | 42 | 39.8 | 16.2 | 442 | 12 | BG789892 |
|   | 43 | 39.6 | 16.2 | 443 | 12 | EG813980 |
|   | 44 | 39.6 | 16.2 | 618 | 13 | B3045011 |
|   | 45 | 39.2 | 16.0 | 606 | 13 | B1479760 |

ALIGNMENTS

AW513637 532 bp mRNA linear EST 03-MAR-2000  
x047h10.x1 NCI-CCAP\_Ut1 Homo sapiens cDNA clone IMAGE:2707171.3,  
similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. ; mRNA  
sequence.

AW513637 1 GI:7151715

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 532)

NCI-CCAP

Unpublished (1997)

Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Email: cyspb-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Sequencing Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing Arrayed by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml



726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 88 a 133 c 158 g 134 t

Query Match 55.0%; Score 134.8; DB 9; Length 513; Best Local Similarity 94.7%; Pred. No. 8.9e-24; Matches 161; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 77 GTCTCCAGTGAAGTGCACAGCCCTGGCGGTGGGAAGTTGGAAGCCAGCTTCACTTC 136

Db 513 GTCTCCAGTGAAGTGCACAGCCCTGGCGGTGGGAAGTTGGAAGCCAGCTTCACTTC 455

QY 137 A-TGAGGAGGAGCGTGCATCCAGAGAAATCTGTATCGGAGAGCGAGAGCGCTGG 195

Db 454 ACTGAGGAGGAGTGTGCTATCCAGAGAAATCTGTATCGGAGAGCGAGAGCGCTGG 395

QY 196 CAATATAGCGCTATGCGGCGAGAGCTCACTGCTACTCTCAGAGCTGC 245

Db 394 CAATATAGCGCTATGCGGCGAGAGCTCACTGCTACTCTCAGAGCTGC 345

RESULT 4 BF193883 337 bp mRNA linear EST 25-APR-2001

LOCUS 245614 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BF193883

VERSION BF193883.1 GI:11077252

KEYWORDS EST.

SOURCE Cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.

REFERENCE 1 (bases 1 to 337)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrnkug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

MEDLINE Genome Res. 11 (4), 626-630 (2001)

COMMENT Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.

PCR PRIMERS FORWARD: AGAAGACGATGATGACAT

BACKWARD: GTTTCACGACGACG

Plate: 76 row: C column: 21

Seq primer: ATTGAGTGACATATAG.

Location/Qualifiers 1. .337

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone\_lib="MARC 2BOV"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 72 a 110 c 110 g 45 t

ORIGIN Query Match 54.9%; Score 134.4; DB 12; Length 337;

Best Local Similarity 75.0%; Pred. No. 9.9e-24; Matches 168; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1 GGAATACACAGGACCTGTACGAGCCATGTGTGATAGGACATTTCCGGAGGA 60

Db 114 GGAATACACAGGACCTGTGTATGAGAGCCATGTGACCGACAGAACTCCCTGAGGA 173

QY 61 CAGAGAGCCACAGAGAGTGTCCCAAGTGAAGTGCAGAGCCCTGGCGGTGGGAAGTTGA 120

Db 174 GATGAGGACCCAGAGAGTGTCCCAAGTGAAGTGCAGAGCCCTGGCGGTGGGAAGTTGA 233

QY 121 AGCCAGCTTCACTTCAATGAGGAGAGATCGGTGCATCCAGAGAAATCTGTATGCGGGA 180

Db 234 ACTCACTGTACCTTCTCTGACAGAGCCCTGCTGCATGAGAGAGATCAAGGCTGACGC 293

QY 181 GACGAGAGGAGCTTGGCAAAATACAGCGCTTATGGGGGCGAGGAAGC 224

Db 294 AACCGGGAGGAGCTTGGCAAAATACAGCTCCAAATGGCGGCAAGAGC 337

RESULT 5 AT251747 477 bp mRNA linear EST 05-NOV-1998

LOCUS Q130F12.X1 Soares\_NFL.T.GBC.S1 Homo sapiens cDNA clone IMAGE1854287/3; similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. 1; mRNA sequence.

ACCESSION AT251747

VERSION AT251747.1 GI:3848276

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 477)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/hiccgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgaps-remail@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 396.

FEATURES 1. .477

Location/Qualifiers /organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1854287"

/clone\_lib="Soares\_NFL.T.GBC.S1"

/lab\_host="DH10B"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.9M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 79 a 123 c 145 g 130 t

ORIGIN Query Match 52.6%; Score 128.8; DB 9; Length 477;

Best Local Similarity 98.5%; Pred. No. 2.8e-22; Matches 130; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 114 AGTTGGAAGCCAGCTTCACTTCAATGAGGAGATCGGTGCATCCAGAGAAATCTGA 173

Db 476 AGTTGGAAGCCAGCTTCACTTCAATGAGGAGATCGGTGCATCCAGAGAAATCTGA 417

QY 174 TCGGAGAGGAGGAGGCTGGCAATACAGCGCCCTATGGGGCAGGAGCTCATGTACC 233  
 |||||  
 Db 416 TCGGAGAGGAGGAGGAGGCTGGCAATACAGCGCCCTATGGGGCAGGAGCTCATGTACC 357  
 |||||  
 QY 234 TGCAGGAGCTGC 245  
 |||||  
 Db 356 TGCAGGAGCTGC 345  
 |||||

RESULT 6  
 R47029 494 bp mRNA linear EST 15-MAY-1995  
 LOCUS Y358 Rat incisor (noncalcified tissues) Rattus norvegicus cDNA  
 DEFINITION clone Y358 5' end similar to odorant-binding protein (RY2G12), mRNA  
 sequence.  
 R47029  
 ACCESSION R47029.1 GI:807371  
 VERSION EST  
 KEYWORDS Norway rat.  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 494)  
 REFERENCE Matsuki,Y., Nakashima,M., Amizuka,N., Warshawsky,H., Goltzman,D.,  
 AUTHORS Yamada,K.M. and Yamada,Y.  
 TITLE A compilation of partial sequences of randomly selected cDNA clones  
 from the rat incisor  
 JOURNAL J. Dent. Res. 74, 307-312 (1995)  
 MEDLINE 95181657  
 COMMENT Contact: Yamada Y  
 Laboratory of Developmental Biology, National Institute of Dental  
 Research  
 NIH/NIH  
 Building 30, Room 405, Bethesda, MD 20892  
 Tel: 3014962111  
 Fax: 3014020897  
 Email: yamadaevoda.nidr.nih.gov  
 Seq primer: AACAAAGCTGGAGCTCCACC.  
 Location/Qualifiers  
 1. 494  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="Y358"  
 /lab\_host="Rat incisor (noncalcified tissues)"  
 /lab\_host="XL-1 blue"  
 /note="Vector: Bluescript II SK-; Site 1: Eco RI; Site 2:  
 Xho I; The apical portion and the entire pulp of the  
 maxillary and mandibular incisors from 3-4 week old rats  
 were excised. A cDNA library was constructed in the lzap  
 II vector (Stratagene) by use of poly A+ RNA from these  
 tissues. The phage cDNA library was converted into a  
 Bluescript phagemid cDNA library by in vivo excision by  
 the ExAssist/SOLR system (Stratagene)."  
 145 a 101 c 144 g 96 t 8 others

BASE COUNT 145 a 101 c 144 g 96 t 8 others  
 ORIGIN

Query Match 39.9%; Score 97.8; DB 14; Length 494;  
 Best Local Similarity 62.4%; Pred. No. 1.7e-14;  
 Matches 153; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1 GGAATACAGAGGAGCTGGTACGTGAGGCCAGCGTGTGTGATAGGACTTCCGGAGGA 60  
 |||||  
 Db 89 GGAATCTCTGGGAAGTGTGTACAGAGGCCAGCGTGTGTGACAGGACACACAGATGG 148  
 |||||  
 QY 61 CAGGAGGCCAGGAGGTGTCCCGAGTGAGGTGACAGCCCTGGCGGTGGGAAGTTGGA 120  
 |||||  
 Db 149 GAAGAGACCTATGAAAGTGTTCCTATGACTGTGACAGCCCTGGGAAGGAGGAGCTTAGA 208  
 |||||  
 QY 121 AGCCAGGTTTCACCTTCATGAGGAGGATCGGTGATCCAGAGAAATCTGTATGCGGAA 180  
 |||||

Db 209 GGTCCGGATAACATTCGGGGGAAGGGTCATTGTCTTTCAGACGAATTACGATGCACA 268  
 |||||  
 QY 181 GAGCGAGAGCGCTGGCAAAATACAGCGCTATGGGGCAGGAGCTCATGTACCTGCAGGA 240  
 |||||  
 Db 269 AACTGATGAGCTGGCGAGTACACTACCTTCAAGGCGCAAGAAGACCTCTATATTAAAGGA 328  
 |||||  
 QY 241 GCTGC 245  
 |||||  
 Db 329 GATTC 333  
 |||||

RESULT 7  
 AA936288 431 bp mRNA linear EST 29-APR-1998  
 LOCUS on75f11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 DEFINITION IMAGE1562541 3' similar to TR:Q63613 Q63613 ODORANT-BINDING  
 PROTEIN. ; mRNA sequence.  
 AA936288  
 ACCESSION AA936288.1 GI:3094206  
 VERSION EST  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 431)  
 REFERENCE NC-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 344.  
 Location/Qualifiers  
 1. 431  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1562541"  
 /lab\_host="DH10B"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NHEK19W, testis NHT, and B-cell  
 NCI-CGAP CGE1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I.M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo.  
 73 a 111 c 136 g 110 t 1 others

BASE COUNT 73 a 111 c 136 g 110 t 1 others  
 ORIGIN

Query Match 37.6%; Score 92.2; DB 9; Length 431;  
 Best Local Similarity 96.9%; Pred. No. 4e-13;  
 Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 149 CGGTGCATCCAGAGAAATCTGTATGGAGAGCGAGGAGCGCTGGCAATACAGGCC 208  
 |||||  
 Db 431 CGGTGCATCCAGAGAAATCTGTATGGAGAGCTGAGGAGCGCTGGCAATACAGGCC 372  
 |||||  
 QY 209 TATGGGGCAGGAGCTCATGTACTGCGAGAGCTGC 245  
 |||||  
 Db 371 TATGGGGCAGGAGCTCATGTACTGCGAGAGCTGC 335  
 |||||

RESULT 8  
 AI877465 519 bp mRNA linear EST 21-JUL-1999  
 LOCUS AI877465







```

Db 64 TCATGTACTCGCAGGAGCTGC 84

RESULT 12
AW920286
LOCUS EST351590 Rat gene index, normalized rat, norvegicus, Bento Soares
DEFINITION Rattus norvegicus cDNA clone RGIG745 5' end, mRNA sequence.
ACCESSION AW920286
VERSION AW920286
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
 Kerlavage,A.R. and Adams,M.D.
TITLE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Unpublished (1998)
COMMENT The Institute for Genomic Research
 9712, Medical Center Drive, Rockville, MD 20850, USA
 Tel: (301)-838-3529
 Fax: (301)-838-0208
 Email: nhlee@tigr.org
 This clone is available through the ATCC, contact the ATCC
 tel#703-365-2700 for further information
 Seq primer: M13 Reverse.

FEATURES Location/Qualifiers
 source 1..594
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /clone_lib="Rat gene index, normalized rat, norvegicus,
 Bento Soares"
 /note="Vector: pBluescript SK(-); site 1. EcoRI; site 2:
 XhoI; estimated insert size approx.1 kb"
BASE COUNT 169 a 153 c 148 g 124 t
ORIGIN
Query Match 28.7%; Score 70.2; DB 10; Length 594;
Best Local Similarity 59.1%; Pred. No. 1.4e-07;
Matches 139; Conservative 0; Mismatches 93; Indels 3; Gaps 1

QY 1 GGATATCATGAGGAGCGTGGTACATGAAGGCCATCGTGTCGTATGACGATTCTCGGAGGA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 93 GGATGTCATGAGGAGCGTGGTATTTGAAATCGCATCGCATGCGCAGGAGATTCCTGACAA 152
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CAGG---AGGCCACCAAGAAGTGTCCCACGTGAAGTGTGACAGCCCTGGCGGTGGGAGGT 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 153 GAAGTTTGAGTGTGTGTGTGACTCCCATGAATATCACGCCCTGGAGGGGGACACT 212
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 118 GGAAGCCACGTTCACTTTCATGAGGGAGGATCGGTGTATCCAGAGAAATTCCTGATGG 177
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 GCAAGTGAAGTTTCACTGTCTGTGATTTTCAGGAGCGTGGCCAGGAGATGAGCACTGTCTG 272
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 GAAGCGGAGGAGCGCTGGCAAATAFACAGCGCTATATGGGGCGAGAGAGCTCATGATC 232
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 GAAGACAGATGAACCTGGCAAATATACAGCGCTATATGTCGCAACAGAGTAGTCTATC 327
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
BM087898
LOCUS BM087898
DEFINITION 500754 MARC 2Bov Bos taurus CDNA 5', mRNA sequence.
ACCESSION BM087898
VERSION BM087898
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubouche,T., Geisel,G., Jost,S.,
 Kucaba,T., Lacy,M., Le,M., Lennon,G., Marra,M., Martin,J., Moore,B.,
 Schellenberg,K., Steptoe,M., Tan,F., Theisinger,B., White,I., Wyllie
 T., Waterston,R. and Wilson.R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLN; contact the
 IMAGE Consortium (info@image.lln.gov) for further information.
 Putative full length read
 The vector to vector length is
 Seq primer: -28m13 rev2 Et from Amersham.

FEATURES Location/Qualifiers
 source 1..415
 /organism="Homo sapiens"
 /db_xref="GDB:6039283"
 /db_xref="taxon:9606"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DHI08"
 /note="Vector: pTTT3D-Pac (Pharmacia) with a modified
 polylinker; site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 Inc., and primed with a Not I - oligo(dT) primer [5',
 TGTTTACCATTGAAGTGGAGCGCGCCCAATTTTTTTTTTTTTTTT 3'].
 Double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pTTT3 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Ronaldo."
BASE COUNT 106 a 134 c 108 g 67 t
ORIGIN
Query Match 32.4%; Score 79.4; DB 9; Length 415;
Best Local Similarity 98.8%; Pred. No. 6.5e-10;
Matches 80; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 165 AAATCTGTATCGGGAAGCAGGAGGAGCGCTTGGCAATATACAGCGCCTATGCGGCGCAGAGC 224
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 AAAAACTGTATCGGGAAGCAGGAGGAGCGCTTGGCAATATACAGCGCCTATGCGGCGCAGAGC 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 225 TCATGTACTCGCAGGAGCTGC 245
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



Search completed: February 10, 2003, 04:58:07  
Job time : 694.035 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:02:40 ; Search time 1097.95 Seconds  
(without alignments)  
8933.518 Million cell updates/sec

Title: 05-09-099-823-3

Perfect score: 337

Sequence: 1 GGGGAGAGAGACTTTATTT.....TAGTGTCCCTCTGGGCGAG 337

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.btg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.in.\*

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19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.btg.hum.\*

31: em.btg.inv.\*

32: em.btg.other.\*

33: em.btg.mus.\*

34: em.btg.pin.\*

35: em.btg.roi.\*

36: em.btg.man.\*

37: em.btg.vit.\*

38: em.sy.\*

39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID         | Description        |
|------------|-------|-------------|--------|----|------------|--------------------|
| C 1        | 335.4 | 99.5        | 739    | 6  | AX454620   | AX454620 Sequence  |
| C 2        | 335.4 | 99.5        | 739    | 6  | AX491098   | AX491098 Sequence  |
| C 3        | 325   | 96.4        | 542    | 6  | AX083548   | AX083548 Sequence  |
| C 4        | 325   | 96.4        | 542    | 6  | AX083548   | AX083548 Sequence  |
| C 5        | 325   | 96.4        | 542    | 6  | AX083548   | AX083548 Sequence  |
| C 6        | 325   | 96.4        | 542    | 6  | AX083548   | AX083548 Sequence  |
| C 7        | 325   | 96.4        | 542    | 6  | AX083548   | AX083548 Sequence  |
| C 8        | 325   | 96.4        | 542    | 6  | AX083548   | AX083548 Sequence  |
| C 9        | 302.6 | 89.8        | 782    | 6  | AX083536   | AX083536 Sequence  |
| C 10       | 302.6 | 89.8        | 782    | 6  | AX083536   | AX083536 Sequence  |
| C 11       | 243.6 | 72.3        | 725    | 6  | AX083538   | AX083538 Sequence  |
| C 12       | 243.6 | 72.3        | 725    | 6  | AX083538   | AX083538 Sequence  |
| C 13       | 240.2 | 71.3        | 607    | 6  | AX083542   | AX083542 Sequence  |
| C 14       | 240.2 | 71.3        | 607    | 6  | AX083542   | AX083542 Sequence  |
| C 15       | 238.6 | 70.8        | 741    | 6  | AX083540   | AX083540 Sequence  |
| C 16       | 238.6 | 70.8        | 741    | 6  | AX083540   | AX083540 Sequence  |
| C 17       | 201   | 59.6        | 522    | 6  | AR204078   | AR204078 Sequence  |
| C 18       | 201   | 59.6        | 522    | 6  | AR204078   | AR204078 Sequence  |
| C 19       | 147   | 43.6        | 510    | 6  | AR204081   | AR204081 Sequence  |
| C 20       | 133   | 39.5        | 13591  | 9  | AX083551   | AX083551 Sequence  |
| C 21       | 133   | 39.5        | 13591  | 9  | AX083551   | AX083551 Sequence  |
| C 22       | 133   | 39.5        | 13591  | 9  | AX083551   | AX083551 Sequence  |
| C 23       | 133   | 39.5        | 13591  | 9  | AX083551   | AX083551 Sequence  |
| C 24       | 131.4 | 39.0        | 87503  | 2  | AC002098   | AC002098 Genomic s |
| C 25       | 131.4 | 39.0        | 87503  | 2  | AC002098   | AC002098 Genomic s |
| C 26       | 129.8 | 38.5        | 10664  | 6  | AX083550   | AX083550 Sequence  |
| C 27       | 129.8 | 38.5        | 10664  | 6  | AX083550   | AX083550 Sequence  |
| C 28       | 129.8 | 38.5        | 10664  | 6  | AX083550   | AX083550 Sequence  |
| C 29       | 129.8 | 38.5        | 10664  | 6  | AX083550   | AX083550 Sequence  |
| C 30       | 105.2 | 31.2        | 539    | 9  | HS214532   | HS214532 Sequence  |
| C 31       | 82.6  | 24.5        | 784    | 9  | HUMHTP     | M76734 Rat odorant |
| C 32       | 81.4  | 24.2        | 732    | 10 | RATTIG21A  | EC027556 Mus muscu |
| C 33       | 79    | 23.4        | 738    | 10 | BC027556   | X62418 H.sapiens m |
| C 34       | 78.8  | 23.4        | 748    | 9  | HSVDEP     | AX214532 Sequence  |
| C 35       | 78.8  | 23.4        | 770    | 6  | AX214532   | AX214532 Sequence  |
| C 36       | 78.8  | 23.4        | 770    | 6  | AX214532   | AX214532 Sequence  |
| C 37       | 73.4  | 21.8        | 525    | 4  | AF027177   | AF027177 Canis fam |
| C 38       | 73.4  | 21.8        | 525    | 4  | AF027177   | AF027177 Canis fam |
| C 39       | 72    | 21.4        | 774    | 6  | E11541     | E11541 Mouse cDNA  |
| C 40       | 72    | 21.4        | 774    | 6  | E11541     | E11541 Mouse cDNA  |
| C 41       | 70.4  | 20.9        | 751    | 10 | MUSVNSPIIB | D38581 Mouse mRNA  |
| C 42       | 70.4  | 20.9        | 751    | 10 | MUSVNSPIIB | D38581 Mouse mRNA  |
| C 43       | 67.4  | 20.0        | 719    | 4  | S77587     | X52016 R.norvegicu |
| C 44       | 65.4  | 19.4        | 147    | 6  | AR204091   | S77587 VEG protein |
| C 45       | 61.6  | 18.3        | 843    | 4  | AF319463   | AR204091 Sequence  |
|            |       |             |        |    |            | AF319463 Macropus  |

## ALIGNMENTS

RESULT 1  
AX454620/c  
LOCUS AX454620  
DEFINITION Sequence 205 from Patent WO0208284.  
ACCESSION AX454620  
VERSION AX454620.1  
KEYWORDS GI:21713934  
SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE

1  
Baker K.P., Ferrara, N., Gerber H., Gerritsen M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.



us-09-099-823-3.rge

Mon Feb 10 11:11:49 2003

QY 133 CTTAGTGTTCGGGACGAGCTTCCGCTCTGAGGGGCGTGAAAATGCTCCTCCGAGA 192  
 DB 422 CTTAGTGTTCGGGACGAGCTTCCGCTCTGAGGGGCGTGAAAATGCTCCTCCGAGA 363  
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 QY 253 TCTTACCCACAAGCTTCCCATGTGGAGAGGCCCCCATGTGGTGTCTTTGCGATGAA 312  
 DB 302 TCTTACCCACAAGCTTCCCATGTGGAGAGGCCCCCATGTGGTGTCTTTGCGATGAA 243  
 QY 313 AGATGTAGTGTCTCCTCTCTGGGCGAG 337  
 DB 242 AGATGTAGTGTCTCCTCTCTGGGCGAG 218

RESULT 4  
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 LOCUS Homo sapiens mRNA for putative odorant binding protein bg (OBPIIb)  
 DEFINITION  
 ACCESSION AJ251028  
 VERSION AJ251028.1 GI:6900080  
 KEYWORDS OBPIIb gene; odorant binding protein.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 542)  
 AUTHORS Lacazette, E., Gachon, A.M. and Pitiot, G.  
 TITLE A novel human odorant-binding protein gene family resulting from  
 genomic duplicons at 9q34: differential expression in the oral and  
 genital spheres  
 JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)  
 MEDLINE 20076326  
 PUBMED 10607840  
 REFERENCE 2 (bases 1 to 542)  
 AUTHORS Gachon, A.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
 U384, Université d'Auvergne, Faculté de Médecine, 28, place Henri  
 Dunant, Clermont Ferrand cedex01 63001, FRANCE  
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 QY 73 GTGGTCCGGGCTCTGTCTGTGGTGTAGGCTCTGGAGTGGAGACCCGGGGCTG 132

RESULT 5  
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 LOCUS Sequence 9 from Patent WO0112806.  
 DEFINITION  
 ACCESSION AX083544  
 VERSION AX083544.1 GI:13185354  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 676)  
 AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.  
 TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 JOURNAL Patent: WO 0112806-A 9 22-FEB-2001;  
 Université d'Auvergne (FR) ; Pitiot, Gilles (FR)  
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 QY 133 CTTTATTGGAGTCAGGTCGGTGGAGAGGAGGTCATGGTCGAGGTCAG 192  
 DB 556 CTTTATTGGAGTCAGGTCGGTGGAGAGGAGGTCATGGTCGAGGTCAG 497  
 QY 193 GTCCCTTGGGCTGACCAATTTCTTAATTTCTTCCAGGGCTCCCGGTTGGTATCAGAA 252  
 DB 496 GTCCCTTGGGCTGACCAATTTCTTAATTTCTTCCAGGGCTCCCGGTTGGTATCAGAA 437







|                           |                                                                                                                                                                                     |             |     |        |                 |
|---------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|-----|--------|-----------------|
| LOCUS                     | AX083538                                                                                                                                                                            | 725 bp      | DNA | linear | PAT 28-FEB-2001 |
| DEFINITION                | Sequence 3 from Patent WO0112806.                                                                                                                                                   |             |     |        |                 |
| ACCESSION                 | AX083538                                                                                                                                                                            |             |     |        |                 |
| VERSION                   | AX083538.1                                                                                                                                                                          | GI:13185348 |     |        |                 |
| KEYWORDS                  | human                                                                                                                                                                               |             |     |        |                 |
| SOURCE                    | ORGANISM                                                                                                                                                                            |             |     |        |                 |
|                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                                                        |             |     |        |                 |
| REFERENCE                 | Pilot,G., Gachon,A.M. and Pilot,G. (bases 1 to 725)                                                                                                                                 |             |     |        |                 |
| AUTHORS                   | Iacazette,E., Gachon,A.M. and Pilot,G.                                                                                                                                              |             |     |        |                 |
| TITLE                     | A novel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres                                 |             |     |        |                 |
| JOURNAL                   | Hum. Mol. Genet. 9 (2), 289-301 (2000)                                                                                                                                              |             |     |        |                 |
| MEDLINE                   | 20076326                                                                                                                                                                            |             |     |        |                 |
| PMID                      | 10607840                                                                                                                                                                            |             |     |        |                 |
| REFERENCE                 | 2 (bases 1 to 676)                                                                                                                                                                  |             |     |        |                 |
| AUTHORS                   | Gachon,A.M.                                                                                                                                                                         |             |     |        |                 |
| TITLE                     | Direct Submission                                                                                                                                                                   |             |     |        |                 |
| JOURNAL                   | Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM U84, Universite d'Auvergne - Faculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE |             |     |        |                 |
| FEATURES                  | Location/Qualifiers                                                                                                                                                                 |             |     |        |                 |
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| Best Local Similarity     | 95.78; Pred. No. 1.6e-73;                                                                                                                                                           |             |     |        |                 |
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| QY                        | 133 CTTAGTGTTCGAGACGAGCTCCGCTCTCGAGGGGGCGTGAATAATGTCCTCCGAGA 192                                                                                                                    |             |     |        |                 |
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| QY                        | 313 AGATGATAGTGTCTCTCTGGGCGAG 337                                                                                                                                                   |             |     |        |                 |
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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 725)  
 AUTHORS Lacazette, E., Gachon, A.M. and Pitiot, G.  
 TITLE A novel human odorant-binding protein gene family resulting from  
 genomic duplications at 9q34: differential expression in the oral and  
 genital spheres  
 JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)  
 MEDLINE 20076326  
 PUBMED 10607840  
 REFERENCE 2 (bases 1 to 725)  
 Gachon, A.M.  
 Direct Submission  
 Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
 U384, Université d'Auvergne - Faculté de Médecine, 28, place Henri  
 Dunant, Clermont Perrand cedex01 63001, FRANCE  
 JOURNAL  
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 Db 425 AGTTTCCCATGTGGAGCGAGCGCCCGGCTGCTGCTTTCGCTTGAAGATGAGTGG 366  
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 LOCUS 607 bp DNA linear PAT 28-FEB-2001

DEFINITION Sequence 7 from Patent WO0112806.  
 ACCESSION AX083542  
 VERSION AX083542.1 GI:13185352  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 607)  
 AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.  
 TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 JOURNAL Patent: WO 0112806-A 7 22-FEB-2001;  
 Université d'Auvergne (FR) ; Pitiot, Gilles (FR)  
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 Db 607 CTTATTTCGACTCAGTGGGTGGGACGAGGAGGTCATGGCTGGAGGTAGGTCCAG 548  
 QY 73 GTGGTCCGGGCTCTGTCTGTGTGGTAGGGCTCTGCAGGTGCAGACCGGGGCTG 132  
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 QY 253 TCCTACCCACAAG 265  
 Db 367 TCCTACCTGCAGG 355  
 RESULT 14  
 HS251023/c  
 LOCUS 607 bp mRNA linear PRI 02-FEB-2000  
 DEFINITION Homo sapiens mRNA for putative odorant binding protein ad (OBPIIIa  
 gene).  
 ACCESSION AJ251023  
 VERSION AJ251023.1 GI:6900070  
 KEYWORDS OBPIIIa gene; odorant binding protein.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 607)  
 AUTHORS Lacazette, E., Gachon, A.M. and Pitiot, G.  
 TITLE A novel human odorant-binding protein gene family resulting from  
 genomic duplications at 9q34: differential expression in the oral and  
 genital spheres  
 JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)

MEDLINE 20076326  
PUBMED 10607840  
REFERENCE 2 (bases 1 to 607)  
AUTHORS Gachon A.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
Dunant, Clermont Ferrand cedex 01 63001, FRANCE  
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Query Match 71.38; Score 240.2; DB 9; Length 607;  
Best Local Similarity 96.48; Pred. No. 3.7e-56;  
Matches 245; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 13 CTTTATTGGAGTCAGGTGGGAGCAGGAGGTCATGCTGGAGGTAGTCCAG 72  
Db 607 CTTTATTGGAGTCAGGTGGGAGCAGGAGGTCATGCTGGAGGTAGTCCAG 548  
Qy 73 GTGGTCCGGGCTCTGTGTGGTGGTGGTCTGGAGGTGCGAGCCCGGGGCTG 132  
Db 547 GTGGTCCGGGCTCTGTGTGGTGGTGGTCTGGAGGTGCGAGCCCGGGGCTG 488  
Qy 133 CTTAGTGTTCGGAGCAGCAGCTCCCGTCTGAGGGGCTGAAATGCTCTCCCGAGA 192  
Db 487 CTTAGTGTTCGGAGCAGCAGCTCCCGTCTGAGGGGCTGAAATGCTCTCCCGAGA 428  
Qy 193 GTCCCTTGGCTGCACCAATTTCTTAATTTCTCCAGGCGCTCCCGGTGATCAGAA 252  
Db 427 GTCCCTTGGCTGCACCAATTTCTTAATTTCTCCAGGCGCTCCCGGTGATCAGAA 368  
Qy 253 TCTTACCACCAAG 265  
Db 367 TCTTACCACCAAG 355  
RESULT 15  
AX083540/c  
LOCUS AX083540 741 bp DNA linear PAT 28-FEB-2001  
DEFINITION Sequence 5 from Patent WO0112806.  
ACCESSION AX083540  
VERSION AX083540.1 GI:13185350  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Pitlot, G., Lacazette, E. and Gachon, F.  
TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
uses Chereof  
Polypeptides and Polynucleotides coding for said polypeptides and  
JOURNAL Patent: WO 0112806-A 5 22-FEB-2001;  
Universite d'Auvergne (FR); Pitlot, Gilles (FR)  
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Best Local Similarity 96.48; Pred. No. 1.1e-55;  
Matches 244; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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Db 741 CTTTATTGGAGTCAGGTGGGAGCAGGAGGTCATGCTGGAGGTAGTCCAG 682  
Qy 73 GTGGTCCGGGCTCTGTGTGGTGGTGGTCTGGAGGTGCGAGCCCGGGGCTG 132  
Db 681 GTGGTCCGGGCTCTGTGTGGTGGTGGTCTGGAGGTGCGAGCCCGGGGCTG 622  
Qy 133 CTTAGTGTTCGGAGCAGCAGCTCCCGTCTGAGGGGCTGAAATGCTCTCCCGAGA 192  
Db 621 CTTAGTGTTCGGAGCAGCAGCTCCCGTCTGAGGGGCTGAAATGCTCTCCCGAGA 562  
Qy 193 GTCCCTTGGCTGCACCAATTTCTTAATTTCTCCAGGCGCTCCCGGTGATCAGAA 252  
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Qy 253 TCTTACCACCAAG 265  
Db 501 TCTTACCACCAAG 489  
Search completed: February 10, 2003, 03:12:41  
Job time : 1104.85 secs

GenCore version 5.1.3  
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OK nucleic - nucleic search, using sw model

Run on: February 9, 2003, 19:57:40 ; Search time 123.814 Seconds  
(without alignments)  
6129.540 Million cell updates/sec

Title: US-09-099-823-3  
Perfect score: 337  
Sequence: 1 GGGGAGAGAGCTTTATTT.....TAGTGTGCTCTCTGGGCGAG 337

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

|     |                                                   |
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| 24: | /SID82/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*  |

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | ID       | Description         |
|------------|-------|-------|-------|--------|----------|---------------------|
| 1          | 337   | 100.0 | 337   | 20     | AX07455  | Human BS124 specif  |
| c 2        | 337   | 100.0 | 590   | 21     | AX291770 | Human breast specif |
| c 3        | 337   | 100.0 | 592   | 20     | AX07456  | Human BS124 specif  |
| c 4        | 337   | 100.0 | 692   | 20     | AX07457  | Human BS124 specif  |
| c 5        | 336.2 | 99.8  | 1002  | 20     | AAV08842 | Gene No. 32 encodi  |
| c 6        | 335.8 | 99.6  | 981   | 20     | AAV08845 | Gene No. 32 encodi  |
| c 7        | 335.4 | 99.5  | 738   | 22     | AAF54313 | DNA encoding prote  |
| c 8        | 335.4 | 99.5  | 739   | 21     | AAV56615 | Human PRO1283 prot  |
| c 9        | 335.4 | 99.5  | 739   | 21     | AAA37071 | Human PRO1283 (UNQ  |

|      |       |      |       |    |          |                    |
|------|-------|------|-------|----|----------|--------------------|
| c 10 | 335.4 | 99.5 | 739   | 24 | ABL95663 | Human angiogenesis |
| c 11 | 335.4 | 99.5 | 739   | 24 | ABL88174 | Human PRO1283 cDNA |
| c 12 | 325   | 96.4 | 542   | 22 | AAF80045 | Nucleotide sequenc |
| c 13 | 325   | 96.4 | 676   | 22 | AAF80043 | Nucleotide sequenc |
| c 14 | 325   | 96.4 | 782   | 22 | AAF80044 | Nucleotide sequenc |
| c 15 | 302.6 | 89.8 | 676   | 22 | AAF80039 | Nucleotide sequenc |
| c 16 | 260.2 | 77.2 | 603   | 23 | AA576054 | DNA encoding novel |
| c 17 | 243.6 | 72.3 | 725   | 23 | AAF80040 | Nucleotide sequenc |
| c 18 | 240.2 | 71.3 | 607   | 22 | AAF80042 | Nucleotide sequenc |
| c 19 | 239.4 | 71.0 | 666   | 23 | AA576055 | DNA encoding novel |
| c 20 | 238.6 | 70.8 | 741   | 22 | AAF80041 | Nucleotide sequenc |
| c 21 | 226.6 | 67.2 | 781   | 22 | AAK51815 | Human polynucleoti |
| c 22 | 201   | 59.6 | 522   | 20 | AAK19505 | Human lipocalin ho |
| c 23 | 201   | 59.6 | 523   | 24 | AD351179 | Human 2lipol DNA.  |
| c 24 | 147   | 43.6 | 310   | 20 | AAK19506 | Degenerate lipocal |
| c 25 | 133   | 39.3 | 3932  | 22 | AAK03258 | Human reproductive |
| c 26 | 133   | 39.3 | 3935  | 22 | AAK03257 | Human reproductive |
| c 27 | 133   | 39.5 | 13391 | 22 | AAF80047 | Nucleotide sequenc |
| c 28 | 129.8 | 38.5 | 10664 | 22 | AAF80046 | Nucleotide sequenc |
| c 29 | 78.8  | 23.4 | 770   | 22 | AAH76463 | CDNA corresponding |
| c 30 | 74    | 22.0 | 2598  | 23 | AA593538 | DNA encoding novel |
| c 31 | 73.4  | 21.8 | 525   | 15 | AAQ69950 | CDNA encoding VASP |
| c 32 | 72    | 21.4 | 774   | 17 | AAK35147 | CDNA encoding VASP |
| c 33 | 61    | 18.1 | 702   | 17 | AAK35146 | Human spliced tran |
| c 34 | 60    | 17.8 | 60    | 24 | ABM43681 | Human lipocalin ho |
| c 35 | 49.4  | 14.7 | 51    | 20 | AAK19516 | Human polynucleoti |
| c 36 | 46.2  | 13.7 | 426   | 22 | AAK52799 | Human lipocalin ho |
| c 37 | 44.6  | 13.2 | 432   | 24 | ABA04115 | Human lipocalin ho |
| c 38 | 44.6  | 13.2 | 555   | 24 | ABA04103 | Human lipocalin ho |
| c 39 | 44.6  | 13.2 | 570   | 22 | AAK97910 | Human secreted pro |
| c 40 | 44.6  | 13.2 | 579   | 24 | ABA04107 | Human lipocalin ho |
| c 41 | 44.6  | 13.2 | 597   | 24 | ABA04111 | Human lipocalin ho |
| c 42 | 43    | 12.8 | 762   | 22 | AA521362 | Human cDNA sequenc |
| c 43 | 37.6  | 11.2 | 9646  | 24 | ABL33688 | Human immune syste |
| c 44 | 36.2  | 10.7 | 15899 | 19 | AAV62164 | HSV-2 strain SB5 C |
| c 45 | 36.2  | 10.7 | 16812 | 19 | AAV62175 | HSV-2 strain SB5 C |

ALIGNMENTS

RESULT 1  
AX07455  
ID AX07455 standard; cDNA; 337 BP.  
XX  
AC AX07455;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Human BS124 specific EST clone g2185139.  
XX  
KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
XX EST; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9859049-AL.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-US12862.  
XX  
PR 20-JUN-1997; 97US-0879354.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Billing-medal PA, Cohen M, Colbitts TL, Friedman DN;  
PI Gordon J, Granados ER, Hodges SC, Klass MR, Kratochvil JD;  
PI Russell JC, Scheffel CP, Stroupe SD, Tu H;  
XX  
XX WPI; 1999-105623/09.  
XX  
XX New isolated BS124 polynucleotides and polypeptides - used for



|            |                                                                           |
|------------|---------------------------------------------------------------------------|
| DR         | WFI; 1999-105623/09.                                                      |
| XX         | New isolated BS124 polynucleotides and polypeptides - used for            |
| XX         | detecting, diagnosing, preventing or treating diseases or conditions      |
| PT         | of the breast, such as breast cancer                                      |
| XX         | Claim 11; Page 95; 125pp; English.                                        |
| PS         | The sequence is that of a consensus BS124-specific EST clone.             |
| CC         | It is useful for detecting, diagnosing, staging, preventing               |
| CC         | or treating, or determining predisposition to diseases or                 |
| CC         | conditions of the breast, such as breast cancer.                          |
| XX         | Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;                     |
| SQ         | Query Match 100.0%; Score 337; DB 20; Length 692;                         |
|            | Best Local Similarity 100.0%; Pred. No. 3.7e-87;                          |
|            | Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |
| QY         | 1 GGGGAGAGACACTTATTTGGAGTCAGGTGGTGCGGAGCAGGAAGGCTAFTGCTGGA 60             |
| DB         | 690 GGGGAGAGAGACACTTATTTGGAGTCAGGTGGTGCGGAGCAGGAAGGCTAFTGCTGGA 631        |
| QY         | 61 GGGTAGTCCAGTGGTGCCGGCTCTGTGCTGGTGTAGGTGGGCTCTGAGAGTGCAG 120            |
| DB         | 630 GGGTAGTCCAGTGGTGCCGGCTCTGTGCTGGTGTAGGTGGGCTCTGAGAGTGCAG 571           |
| QY         | 121 ACCCGGGGGCTGCCAGTGTTCGGAGCAGCAGCTCCCGCTCTCAGGGGCGTCAAAATGT 180        |
| DB         | 570 ACCCGGGGGCTGCCAGTGTTCGGAGCAGCAGCTCCCGCTCTCAGGGGCGTCAAAATGT 511        |
| QY         | 181 CCTCTCCGAGAGTCCCTTGGCTGCACCATTCTTAATTTCTCCAGGCGCTCCCGGT 240           |
| DB         | 510 CCTCTCCGAGAGTCCCTTGGCTGCACCATTCTTAATTTCTCCAGGCGCTCCCGGT 451           |
| QY         | 241 TGGTATCAGAATTCCTATCCACAAGCTTCCCATGTGAGCAGGCCCCCATGTGCTGGT 300         |
| DB         | 450 TGGTATCAGAATTCCTATCCACAAGCTTCCCATGTGAGCAGGCCCCCATGTGCTGGT 391         |
| QY         | 301 CTTTGGCAGTAAAGATAGTGTGCTCCCTCTGGGCAG 337                              |
| DB         | 390 CTTTGGCAGTAAAGATAGTGTGCTCCCTCTGGGCAG 354                              |
| RESULT 5   |                                                                           |
| AAV08842/c |                                                                           |
| ID         | AAV08842 standard; cDNA; 1002 BP.                                         |
| XX         | AAV08842;                                                                 |
| AC         | 19-FEB-1999 (first entry)                                                 |
| DT         | Gene No. 32 encoding human secreted protein.                              |
| XX         | Secreted protein; human; protein therapy; gene therapy; blood disorder;   |
| KW         | pathological condition; diagnosis; cancer; neurological disorder;         |
| KW         | developmental abnormality; foetal deficiency; leukaemia; hepatic disease; |
| KW         | immune system disorder; Alzheimer's disease; cognitive disorder;          |
| KW         | schizophrenia; prostate disease; autoimmune disorder; AIDS; ds.           |
| OS         | Homo sapiens.                                                             |
| XX         | W09854206-A1.                                                             |
| PN         | 03-DEC-1998,                                                              |
| PD         | 28-MAY-1998; 98WO-US10868.                                                |
| XX         | 29-AUG-1997; 97US-0056296.                                                |
| PR         | 30-MAY-1997; 97US-004039.                                                 |
| PR         | 30-MAY-1997; 97US-0048093.                                                |
| PR         | 30-MAY-1997; 97US-0048101.                                                |
| PR         | 30-MAY-1997; 97US-0048190.                                                |

DR WPI; 1999-105623/09.

XX New isolated BS124 polynucleotides and polypeptides - used for

PT detecting, diagnosing, preventing or treating diseases or conditions

PT of the breast, such as breast cancer

XX Claim 11; Pages 94-95; 125pp; English.

PS The sequence is that of a BS124-specific EST clone.

CC It is useful for detecting, diagnosing, staging, preventing

CC or treating, or determining predisposition to diseases or

CC conditions of the breast, such as breast cancer.

XX Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;

SQ

Query Match 100.0%; Score 337; DB 20; Length 692;  
Best Local Similarity 100.0%; Pred. No. 3.7e-87;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCGGAGAGACCTTATTGGAGTCAGGTGGGTGGGAGCAGGGAAGGTCATGGCTGGA 60  
Db 690 GGCGGAGAGAGACTTTATTGGAGTCAGGTGGGTGGGAGCAGGGAAGGTCATGGCTGGA 631  
QY 61 GGGTAGGTCCAGGTGTCGGGGCTCTGTGCTGGTGAGGTGGCTCTCGAGGTGCAG 120  
Db 630 GGGTAGGTCCAGGTGTCGGGGCTCTGTGCTGGTGAGGTGGCTCTCGAGGTGCAG 571  
QY 121 ACCCGGGGGGCTGCCTAGTGTTCGGGAAACGACGTCGCCGCTCGAGGGCGTGAAAATGT 180  
Db 570 ACCCGGGGGGCTGCCTAGTGTTCGGGAAACGACGTCGCCGCTCGAGGGCGTGAAAATGT 511  
QY 181 CCTCTCTCGAGAGTCCCTTGGCGTGTGCACCATAATTTCTTAATTCCTCAGGGCTGCCCGT 240  
Db 510 CTCTCTCGAGAGTCCCTTGGCGTGTGCACCATAATTTCTTAATTCCTCAGGGCTGCCCGT 451  
QY 241 TGCTFNCAGATTCTCAACCAAGCTTTCCCATGTGGAGCAGGCCCCCATTGGTGTGTGT 300  
Db 450 TGGTTCAGAAATCTCAACCAAGCTTTCCCATGTGGAGCAGGCCCCCATTGGTGTGTGT 391  
QY 301 CTTTCGAGTAAAGAGTAGTGGTCCCTCTGGGCAG 337  
Db 390 CTTTCGAGTAAAGAGTAGTGGTCCCTCTGGGCAG 354

RESULT 4  
AAX07457/c  
ID AAX07457 standard; cDNA; 692 BP.  
XX AC AAX07457;  
XX DT 08-JUN-1999 (first entry)  
DE Human BS124 specific EST clone consensus sequence.  
XX BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
KW consenus; EST; ss.  
XX Homo sapiens.  
PN WO9859049-A1.  
XX PD 30-DEC-1998.  
PF 19-JUN-1998; 98WO-US12862.  
XX PR 20-JUN-1997; 97US-0879354.  
XX PA (ABSO ) ABBOTT LAB.  
XX Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;  
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
PI Russell JC, Scheffel CP, Stroupe SD, Yu H;  
XX









[illegible]







Query Match 96.4%; Score 325; DB 22; Length 782;  
Best local similarity 100.0%; Pred. No. 1.1e-83;



Mon Feb 10 11:11:50 2003

deodorants etc.. OBP polypeptides are used as binding proteins for  
hydrophobic ligands (particularly odorants); as competitive inhibitors  
(agonists or antagonists) of cellular lipocalin receptors; to detect  
specific antibodies for diagnosis of allergy, asthma or cancer; for  
controlling volatilisation of an odorant, specifically in perfumes,  
cosmetics or disinfectant compositions; to screen compounds, especially  
odorants or flavours, e.g. human pheromones, for binding to OBP, also in  
analysis of complex perfume mixtures; to solubilise lipophilic compounds;  
for treating hyperlipidemia or obesity, or to supplement non-maternal  
milk when combined with nutritional fatty acids, as food additives; as a  
transporter of pharmaceuticals, especially anticancer agents (providing  
delayed release) but also for delivery across the placental barrier  
(e.g. for detoxification of the foetus); as a marker of pregnancy or  
foeto-placental pathology (rupture of the amniotic membrane); and as  
antiallergic agents.

XX Sequence 676 BP; 158 A; 199 C; 204 G; 115 T; 0 other;

Query Match 89.8%; Score 302.6; DB 22; Length 676;  
Best Local Similarity 95.7%; Pred. No. 2.9e-77;  
Matches 311; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 13 CTTTATTGGAGTCAGTGGTGGGACGAGGAGGATCATGGCTGGAGGGTAGTCCAG 72  
DB 676 CTTTATTGGAGTCAGTGGTGGGACGAGGAGGATCATGGCTGGAGGGTAGTCCAG 617  
QY 73 GTGGTCCGGGCTCTGTCTGTGTGTAGGGTGGGCTCTGGAGGTGCAGACCCGGGGCTG 132  
DB 616 GTGGTCCGGGCTCTGTCTGTGTGTAGGGTGGGCTCTGGAGGTGCAGACCCGGGGCTG 557  
QY 133 CCTAGTGTTCGGGACGACGCTCCCGTCTGTCAGGGGCGTGAAAATGCTCTCTCCGAGA 192  
DB 556 CCTAGTGTTCGGGACGACGCTCCCGTCTGTCAGGGGCGTGAAAATGCTCTCTCCGAGA 497  
QY 193 GTCCCTTGGGCTGCACCAATTTCTTAATTTCTCCAGGGCTCCCGTGTGGTATCAGAA 252  
DB 496 GTCCCTTGGGCTGCACCAATTTCTTAATTTCTCCAGGGCTCCCGTGTGGTATCAGAA 437  
QY 253 TCCTACCCACAGCTTCCCAATGGGACGAGCCGCCCATGGTGGTGTTCGACTAAA 312  
DB 436 TCCTACCCACAGCTTCCCAATGGGACGAGCCGCCCATGGTGGTGTTCGACTAAA 377  
QY 313 AGATGTAGTGGTCCCTCTGGGCGAG 337  
DB 376 AGATGTAGTGGTCCCTCTGGGCGAG 352

Search completed: February 9, 2003, 22:02:18  
Job time : 131.814 secs

Mon Feb 10 11:11:51 2003

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 20:30:25 ; Search time 24.4956 Seconds  
(without alignments)  
4219.129 Million cell updates/sec

Title: US-09-099-823-3  
Perfect score: 337  
Sequence: 1 GGGGAGAGGACTTTAATT.....TAGTGGTCCCTCTGGGCG 337  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues  
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description      |
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| C 1        | 201   | 59.6        | 522    | 3  | US-09-130-663-1  |
| C 2        | 201   | 59.6        | 522    | 3  | US-09-432-335-1  |
| C 3        | 201   | 59.6        | 522    | 3  | US-09-614-022-1  |
| C 4        | 147   | 43.6        | 510    | 3  | US-09-130-663-5  |
| C 5        | 147   | 43.6        | 510    | 3  | US-09-432-335-5  |
| C 6        | 147   | 43.6        | 510    | 4  | US-09-614-022-5  |
| C 7        | 73.4  | 21.8        | 525    | 2  | US-08-467-793-1  |
| C 8        | 73.4  | 21.8        | 525    | 2  | US-08-466-793-1  |
| C 9        | 73.4  | 21.8        | 525    | 2  | US-08-491-861A-1 |
| C 10       | 65.4  | 19.4        | 147    | 3  | US-09-130-663-17 |
| C 11       | 65.4  | 19.4        | 147    | 3  | US-09-432-335-17 |
| C 12       | 65.4  | 19.4        | 147    | 4  | US-09-614-022-17 |
| C 13       | 49.4  | 14.7        | 51     | 3  | US-09-130-663-19 |
| C 14       | 49.4  | 14.7        | 51     | 3  | US-09-432-335-19 |
| C 15       | 49.4  | 14.7        | 51     | 4  | US-09-614-022-19 |
| C 16       | 35.4  | 10.5        | 63     | 3  | US-09-130-663-20 |
| C 17       | 35.4  | 10.5        | 63     | 3  | US-09-432-335-20 |
| C 18       | 35.4  | 10.5        | 63     | 3  | US-08-614-022-20 |
| C 19       | 34    | 10.1        | 827    | 1  | US-08-726-723-3  |
| C 20       | 33.4  | 9.9         | 1190   | 1  | US-08-310-370-1  |
| C 21       | 33    | 9.8         | 3065   | 2  | US-08-209-521-28 |
| C 22       | 32.8  | 9.7         | 888    | 4  | US-08-765-907A-2 |
| C 23       | 32.8  | 9.7         | 2888   | 4  | US-08-765-907A-1 |
| C 24       | 32.6  | 9.7         | 5159   | 2  | US-08-146-930-3  |
| C 25       | 32.6  | 9.7         | 5159   | 5  | US-08-458-240-3  |
| C 26       | 32.6  | 9.7         | 5159   | 5  | PCT-US93-03993-3 |
| C 27       | 32.2  | 9.6         | 1833   | 2  | US-08-403-852D-6 |

|      |      |     |         |   |                  |
|------|------|-----|---------|---|------------------|
| C 28 | 32.2 | 9.6 | 1833    | 3 | US-08-510-646B-6 |
| C 29 | 32.2 | 9.6 | 1833    | 4 | US-09-231-818-6  |
| C 30 | 31.8 | 9.4 | 319     | 4 | US-09-165-264-8  |
| C 31 | 31.8 | 9.4 | 7218    | 1 | US-08-232-463-14 |
| C 32 | 31.6 | 9.4 | 289     | 4 | US-09-007-005-17 |
| C 33 | 31.6 | 9.4 | 289     | 4 | US-09-244-796-17 |
| C 34 | 31.6 | 9.4 | 1419    | 4 | US-09-276-531-1  |
| C 35 | 31.6 | 9.4 | 9278    | 1 | US-08-243-542-9  |
| C 36 | 31.6 | 9.4 | 9278    | 1 | US-08-477-407-9  |
| C 37 | 31.6 | 9.4 | 9278    | 1 | US-08-484-355-9  |
| C 38 | 31.4 | 9.3 | 955     | 4 | US-09-641-638-23 |
| C 39 | 31.4 | 9.3 | 955     | 4 | US-09-641-638-24 |
| C 40 | 31.4 | 9.3 | 4411529 | 4 | US-09-103-840A-1 |
| C 41 | 31   | 9.2 | 289     | 4 | US-09-007-005-17 |
| C 42 | 31   | 9.2 | 289     | 4 | US-09-244-796-17 |
| C 43 | 31   | 9.2 | 318     | 4 | US-09-165-264-12 |
| C 44 | 31   | 9.2 | 448     | 4 | US-09-060-756-64 |
| C 45 | 31   | 9.2 | 35060   | 3 | US-08-814-095-7  |

ALIGNMENTS

RESULT 1  
US-09-130-663-1/c  
; Sequence 1, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)...(516)  
US-09-130-663-1

|                       |                                                                |                    |               |             |
|-----------------------|----------------------------------------------------------------|--------------------|---------------|-------------|
| Query Match           | 59.6%                                                          | Score 201;         | DB 3;         | Length 522; |
| Best Local Similarity | 100.0%;                                                        | Pred. No. 2.6e-50; | Mismatches 0; | Indels 0;   |
| Matches 201;          | Conservative 0;                                                |                    |               |             |
| QY 137                | GTGTTGCGGGAACGACAGTTCCTCCGCTCTCGAGGGGCGTGAAATGTCCTCCGCGAGAGTCC | 196                |               |             |
| DB 516                | GTGTTGCGGGAACGACAGTTCCTCCGCTCTCGAGGGGCGTGAAATGTCCTCCGCGAGAGTCC | 457                |               |             |
| QY 197                | CTTGGCGTGCACCAATTCCTAAATTTCTCCAGGCGCTCCCGTGTGATATCAGATTCCT     | 256                |               |             |
| DB 456                | CTTGGCGTGCACCAATTCCTAAATTTCTCCAGGCGCTCCCGTGTGATATCAGATTCCT     | 397                |               |             |
| QY 257                | ACCCACAGCTTTCCTCCATGCGAGGAGCGGCCGCCATGCTGTGCTTTTCAGTAAAGAT     | 316                |               |             |
| DB 396                | ACCCACAGCTTTCCTCCATGCGAGGAGCGGCCGCCATGCTGTGCTTTTCAGTAAAGAT     | 337                |               |             |
| QY 317                | GTAGTGTGTCCTCTGGGCGAG 337                                      |                    |               |             |
| DB 336                | GTAGTGTGTCCTCTGGGCGAG 316                                      |                    |               |             |

RESULT 2  
US-09-432-335-1/c  
; Sequence 1, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.

197 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 256  
456 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 397  
257 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 316  
396 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 337  
317 GTAGTGTCTCTCTCTGGGCGAG 337  
336 GTAGTGTCTCTCTGGGCGAG 316

RESULT 4  
US-09-130-663-5/c  
; Sequence 5, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 510  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate sequence derived from human zlipol1  
; OTHER INFORMATION: nucleotide sequence  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (1)...(510)  
; OTHER INFORMATION: n is any nucleotide  
US-09-130-663-5

Query Match 43.6%; Score 147; DB 3; Length 510;  
Best Local Similarity 57.7%; Pred. No. 2.3e-34;  
Matches 116; Conservative 53; Mismatches 32; Indels 0; Gaps 0;  
137 GTGTTGGGGAACGAGCTTCCGCTCTGCAGGGCGTGAATAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 196  
510 RTGYTCNGGNACRCANSWNCNGTTCGNARNGNGTAAADATRTCTCTCTCNSNARNC 451  
197 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 256  
450 YTTCKYTGACNARYTTTAAATTTCTTCNARNGCYTCNCKRTTGTCTCNSWRTNCK 391  
257 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 316  
390 NCCNACNARTTTCACATTCNARNGNARNCNCCRTGTGTGTCTCTTCATTAADAT 331  
317 GTAGTGTCTCTCTGGGCGAG 337  
330 RTAGTGTCTCCKCKNGGNAR 310

RESULT 5  
US-09-432-335-5/c  
; Sequence 5, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; CURRENT FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06

197 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 256  
456 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 397  
257 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 316  
396 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 337  
317 GTAGTGTCTCTCTGGGCGAG 337  
336 GTAGTGTCTCTGGGCGAG 316

RESULT 4  
US-09-130-663-5/c  
; Sequence 5, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)...(516)  
US-09-432-335-1

Query Match 59.6%; Score 201; DB 3; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.6e-50;  
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
137 GTGTTGGGGAACGAGCTTCCCGCTCTGCAGGGCGTGAATAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 196  
516 GTGTTGGGGAACGAGCTTCCCGCTCTGCAGGGCGTGAATAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 397  
197 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 256  
456 CTTGCGCTGCACCAATTTCTTAAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 397  
257 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 316  
396 ACCCACAAGCTTTCCCATGTGGAGCAGGCCGCCCATGCGTGTCTTTGCGAGTAAAGAT 337  
317 GTAGTGTCTCTCTGGGCGAG 337  
336 GTAGTGTCTCTGGGCGAG 316

RESULT 3  
US-09-614-022-1/c  
; Sequence 1, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/054,867  
; PRIOR FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)...(516)  
US-09-614-022-1

Query Match 59.6%; Score 201; DB 4; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.6e-50;  
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
137 GTGTTGGGGAACGAGCTTCCCGCTCTGCAGGGCGTGAATAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 196  
516 GTGTTGGGGAACGAGCTTCCCGCTCTGCAGGGCGTGAATAATTTCTTCAGGGCTCCCGGTGGTATCAGAAATTCCT 457



QY 140 TTCGGAGACGAGCTCCCTGTCGAGGGCGGTGAATGCTCTCCCTCGAGAGTCCCTT 199  
Db 516 TCTGAGAGAGGTTTGGCTCTGCGGAGTTCCTCAAAATCTCTGGTTC---AATCCTT 460  
QY 200 GCCTGTCACGATTTCTTAATCTTCAGGCGCTCCCGGTGTGATFAGAGATTCCTAC 259  
Db 459 GGCCTTGAGATTCCTCAAAATCTCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 400  
QY 260 CACAAGCTTCCCATGTGAGCAGAGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 319  
Db 399 CAGAAGCTTGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340  
QY 320 GTGCTCCCTCTGCG 334  
Db 339 GTGCTCCCTCACCG 325

## RESULT 8

US-08-466-793-1/C  
; Sequence 1, Application US/08466793  
; Patent No. 5891716  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanieczny, Andrey  
; APPLICANT: Bizindaukas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
; TITLE OF INVENTION: Peptides from Dog  
; TITLE OF INVENTION: Dander and Uses Therefor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,793  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/156,549  
; FILING DATE: 22-NOV-1993  
; APPLICATION NUMBER: 07/999,712  
; FILING DATE: 31-Dec-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-5941  
; TELEFAX: (617) 227-7400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 525 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..525  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 79..525  
US-08-466-793-1

Query Match 21.88; Score 73.4; DB 2; Length 525;  
Best Local Similarity 64.68; Pred. NO. 1.2e-12;  
Matches 126; Conservative 0; Mismatches 66; Indels 3; Gaps 1;  
QY 140 TTCGGAGACGAGCTTCCTGTCGAGGGCGGTGAATGCTCTCCCTCGAGAGTCCCTT 199  
Db 516 TCTGAGAGAGGTTTGGCTCTGCGGAGTTCCTCAAAATCTCTGGTTC---AATCCTT 460  
QY 200 GCCTGTCACGATTTCTTAATCTTCAGGCGCTCCCGGTGTGATFAGAGATTCCTAC 259  
Db 459 GGCCTTGAGATTCCTCAAAATCTCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 400  
QY 260 CACAAGCTTCCCATGTGAGCAGAGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 319  
Db 399 CAGAAGCTTGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340  
QY 320 GTGCTCCCTCTGCG 334  
Db 339 GTGCTCCCTCACCG 325  
RESULT 9  
US-08-491-861A-1/C  
; Sequence 1, Application US/08491861A  
; Patent No. 5939283  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanieczny, Andrey  
; APPLICANT: Bizindaukas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
; TITLE OF INVENTION: Dander and Uses Therefor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/491,861A  
; FILING DATE: 27-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/999,712  
; FILING DATE: 31-Dec-92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 525 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..525  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 79..525

## US-08-491-861A-1

Query Match 21.8%; Score 73.4; DB 2; Length 525;  
Best Local Similarity 64.6%; Pred. No. 1.2e-12;  
Matches 126; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 140 TTGCGACACGCTTCCGTCGAGGGCGTGAATGCTCTCTCCGAGAGTCCTCTT 199  
Db 516 TCTGAGAGAGTTGCTCTGCGGAGTTCGAAATCTCTCTGCTC---AATCTTT 460  
QY 200 GCGTCGACCAATTCCTTAATCTTCAGGGCTCCCGTGTGTATGATGATGCTTACC 259  
Db 459 GCGTTTGAGATTCGGAATATCTCCAGGCTCTTGGCTGTCTCAGGATCCCTTCC 400  
QY 260 CACAGCTTTCCCATGTGAGAGCGCCCATGCTGTGTCTGCTTTCAGATAAAGATGA 319  
Db 399 CAGAGCTGGCATTCGGATCTGCTCCCATGAGTCCGCTCCGCTAGAGATGTA 340  
QY 320 GTGCTCCTCTGG 334  
Db 339 GTGCTCCTCACCG 325

## RESULT 10

US-09-130-663-17/c  
; Sequence 17, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-terminal 3' linker  
US-09-130-663-17

Query Match 19.4%; Score 65.4; DB 3; Length 147;  
Best Local Similarity 98.5%; Pred. No. 1.8e-10;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 136 AGTGTCGGAGACGACGCTTCCGCTCTGAGGGCGTGAAATGCTCTCTCCGAGAGTC 195  
Db 67 AGTGTCGGAGACGACGCTTCCGCTCTGAGGGAGTGAAATGCTCTCTCCGAGAGTC 8  
QY 196 CCTTGGC 202  
Db 7 CCTTGGC 1

## RESULT 11

US-09-432-335-17/c  
; Sequence 17, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; CURRENT FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-terminal 3' linker  
US-09-432-335-17

Query Match 19.4%; Score 65.4; DB 3; Length 147;  
Best Local Similarity 98.5%; Pred. No. 1.8e-10;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 136 AGTGTCGGAGACGACGCTTCCGCTCTGAGGGCGTGAAATGCTCTCTCCGAGAGTC 195  
Db 67 AGTGTCGGAGACGACGCTTCCGCTCTGAGGGAGTGAAATGCTCTCTCCGAGAGTC 8  
QY 196 CCTTGGC 202  
Db 7 CCTTGGC 1

## RESULT 12

US-09-614-022-17/c  
; Sequence 17, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/054,867  
; PRIOR FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-terminal 3' linker  
US-09-614-022-17

Query Match 19.4%; Score 65.4; DB 4; Length 147;  
Best Local Similarity 98.5%; Pred. No. 1.8e-10;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 136 AGTGTCGGAGACGACGCTTCCGCTCTGAGGGCGTGAAATGCTCTCTCCGAGAGTC 195  
Db 67 AGTGTCGGAGACGACGCTTCCGCTCTGAGGGAGTGAAATGCTCTCTCCGAGAGTC 8  
QY 196 CCTTGGC 202  
Db 7 CCTTGGC 1

## RESULT 13

US-09-130-663-19/c  
; Sequence 19, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0

Mon Feb 10 11:11:51 2003

us-09-099-823-3.rni

Page 6

; SEQ ID NO 19  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer: ZC13727  
US-09-130-663-19

Query Match 14.7%; Score 49.4; DB 3; Length 51;  
Best Local Similarity 98.0%; Pred. No. 6.2e-06;  
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 152 GCTTCCCGTCTGCAGGGGCGTGAATAATGTCCTCTCCGAGAGTCCCTTGGC 202  
|||||  
Db 51 GCTTCCCGTCTGCAGGGGCGTGAATAATGTCCTCTCCGAGAGTCCCTTGGC 1

RESULT 14  
US-09-432-335-19/c  
; Sequence 19, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; CURRENT FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer: ZC13727  
US-09-432-335-19

Query Match 14.7%; Score 49.4; DB 3; Length 51;  
Best Local Similarity 98.0%; Pred. No. 6.2e-06;  
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 152 GCTTCCCGTCTGCAGGGGCGTGAATAATGTCCTCTCCGAGAGTCCCTTGGC 202  
|||||  
Db 51 GCTTCCCGTCTGCAGGGGCGTGAATAATGTCCTCTCCGAGAGTCCCTTGGC 1

RESULT 15  
US-09-614-022-19/c  
; Sequence 19, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/054,867  
; PRIOR FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer: ZC13727  
US-09-614-022-19

Query Match 14.7%; Score 49.4; DB 4; Length 51;  
Best Local Similarity 98.0%; Pred. No. 6.2e-06;  
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 51 GCTTCCCGTCTGCAGGGGCGTGAATAATGTCCTCTCCGAGAGTCCCTTGGC 1  
Search completed: February 9, 2003, 22:05:13  
Job time : 32.4956 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: February 9, 2003, 21:14:50 ; Search time 25 9802 Seconds  
(without alignments)  
5148.496 Million cell updates/sec

Title: US-09-099-823-3  
Perfect score: 337  
Sequence: 1 GGGGGAGAGGACCTTATTT.....TAGVGTCCCTCTGGGCG 337

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0  
Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq:\*  
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14: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                          |
|------------|-------|-------------|--------|----|--------------------------------------|
| 1          | 337   | 100.0       | 337    | 10 | US-09-099-823-3 Sequence 3, Appli    |
| 2          | 337   | 100.0       | 501    | 10 | US-09-833-381-803 Sequence 803, App  |
| 3          | 337   | 100.0       | 692    | 10 | US-09-099-823-4 Sequence 4, Appli    |
| 4          | 337   | 100.0       | 692    | 10 | US-09-099-823-5 Sequence 5, Appli    |
| 5          | 201   | 59.6        | 523    | 10 | US-09-951-845-1 Sequence 1, Appli    |
| 6          | 73.4  | 21.8        | 525    | 10 | US-09-374-671-1 Sequence 1, Appli    |
| 7          | 44.6  | 13.2        | 432    | 9  | US-09-854-847-25 Sequence 25, Appl   |
| 8          | 44.6  | 13.2        | 555    | 9  | US-10-143-576-1 Sequence 1, Appli    |
| 9          | 44.6  | 13.2        | 555    | 10 | US-09-854-847-1 Sequence 1, Appli    |
| 10         | 44.6  | 13.2        | 570    | 10 | US-09-800-729-37 Sequence 37, Appl   |
| 11         | 44.6  | 13.2        | 579    | 10 | US-09-854-847-9 Sequence 9, Appli    |
| 12         | 44.6  | 13.2        | 597    | 10 | US-09-854-847-17 Sequence 17, Appl   |
| 13         | 43    | 12.8        | 762    | 9  | US-10-028-072-237 Sequence 237, App  |
| 14         | 43    | 12.8        | 762    | 9  | US-10-121-049-237 Sequence 237, App  |
| 15         | 43    | 12.8        | 762    | 9  | US-10-123-304-237 Sequence 237, App  |
| 16         | 43    | 12.8        | 762    | 9  | US-10-140-470-237 Sequence 237, App  |
| 17         | 38.2  | 11.3        | 504    | 10 | US-09-878-574-4330 Sequence 4330, Ap |
| 18         | 36.2  | 10.7        | 3502   | 10 | US-09-880-192-37 Sequence 37, Appl   |
| 19         | 35.6  | 10.6        | 1434   | 10 | US-09-822-830A-53 Sequence 53, Appl  |

ALIGNMENTS

RESULT 1  
US-09-099-823-3  
Sequence 3, Application US/09099823  
Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRADNOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JOHN D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESS: Abbott Laboratories  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.

Sequence 80, Appl  
Sequence 81, Appl  
Sequence 521, App  
Sequence 840, App  
Sequence 2589, Ap  
Sequence 341, App  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 1645, Ap  
Sequence 2, Appli  
Sequence 6802, Ap  
Sequence 931, App  
Sequence 8, Appli  
Sequence 7680, Ap  
Sequence 302, App  
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Sequence 181, App  
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Sequence 181, App

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1605 9 US-09-989-920-81  
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2000 10 US-09-887-576-840  
477 9 US-09-938-842A-2589  
681 10 US-09-770-149-341  
10968 10 US-09-867-753-3  
42450 10 US-09-815-048-3  
1176 10 US-09-917-800A-1645  
33675 10 US-09-921-992-2  
404 10 US-09-960-352-6802  
606 10 US-09-917-800A-931  
1545 9 US-09-712-353-8  
351 10 US-09-960-352-7680  
1533 9 US-09-978-295A-302  
1533 9 US-09-978-697-302  
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1533 9 US-10-175-738-181  
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1533 9 US-10-176-482-181





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US-09-099-823-4
Query Match 100.0%; Score 337; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.3e-89;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 690 GGGGAGAGAGACTTTATTGGAGTCAGTGGGTGGGAGCAGGAGGTCATGCTGGA 631

QY 61 GGGTAGGTCCAGTGGTCCGGGCTCTGTGTCGTGGTAGGTGGGCTCTGGAGTGCAG 120
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Db 630 GGGTAGGTCCAGTGGTCCGGGCTCTGTGTCGTGGTAGGTGGGCTCTGGAGTGCAG 571

QY 121 ACCCGGGGCTGGCTAGTGTTCGGGAACGACAGTTCCTCCGTCGACAGGGGCTCCCGGT 180
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Db 570 ACCCGGGGCTGGCTAGTGTTCGGGAACGACAGTTCCTCCGTCGACAGGGGCTCCCGGT 511

QY 181 CCTCTCCGAGAGTCCCTTCGCGCTGCACCAATTTCTTAATTTCTCCAGGGCTCCCGGT 240
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Db 510 CCTCTCCGAGAGTCCCTTCGCGCTGCACCAATTTCTTAATTTCTCCAGGGCTCCCGGT 451

QY 241 TGGTATCAGATTCCTACCCACAGCTTCCCATGTGGAGCAGGCCGCCCATGCTGCTGT 300
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Db 450 TGGTATCAGATTCCTACCCACAGCTTCCCATGTGGAGCAGGCCGCCCATGCTGCTGT 391

QY 301 CTTTGCAGTAAAGATAGTGTCCCTCCCTGGGCGAG 337
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Db 390 CTTTGCAGTAAAGATAGTGTCCCTCCCTGGGCGAG 354

RESULT 4
US-09-099-823-5/c
; Sequence 5, Application US/09099823
; Patent No. US2002018990A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON JULIAN
; APPLICANT: GRANADOS EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: SCHEFFEL, CHRISTI
; APPLICANT: STROUPE, STEPHEN D.
; APPLICANT: YU, HONG
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,823
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,354
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.

US-09-099-823-5
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6120, US, PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-099-823-5
Query Match 100.0%; Score 337; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.3e-89;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGAGAGAGACTTTATTGGAGTCAGTGGGTGGGAGCAGGAGGTCATGCTGGA 60
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QY 61 GGGTAGGTCCAGTGGTCCGGGCTCTGTGTCGTGGTAGGTGGGCTCTGGAGTGCAG 120
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Db 630 GGGTAGGTCCAGTGGTCCGGGCTCTGTGTCGTGGTAGGTGGGCTCTGGAGTGCAG 571

QY 121 ACCCGGGGCTGGCTAGTGTTCGGGAACGACAGTTCCTCCGTCGACAGGGGCTCCCGGT 180
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Db 570 ACCCGGGGCTGGCTAGTGTTCGGGAACGACAGTTCCTCCGTCGACAGGGGCTCCCGGT 511

QY 181 CCTCTCCGAGAGTCCCTTCGCGCTGCACCAATTTCTTAATTTCTCCAGGGCTCCCGGT 240
 |||||||
Db 510 CCTCTCCGAGAGTCCCTTCGCGCTGCACCAATTTCTTAATTTCTCCAGGGCTCCCGGT 451

QY 241 TGGTATCAGATTCCTACCCACAGCTTCCCATGTGGAGCAGGCCGCCCATGCTGCTGT 300
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Db 450 TGGTATCAGATTCCTACCCACAGCTTCCCATGTGGAGCAGGCCGCCCATGCTGCTGT 391

QY 301 CTTTGCAGTAAAGATAGTGTCCCTCCCTGGGCGAG 337
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Db 390 CTTTGCAGTAAAGATAGTGTCCCTCCCTGGGCGAG 354

RESULT 5
US-09-951-845-1/c
; Sequence 1, Application US/09951845
; Patent No. US20020098497A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Foster, Donald C.
; APPLICANT: Holloway, James L.
; TITLE OF INVENTION: Use of Human Phormone Polypeptides
; FILE REFERENCE: 00-85
; CURRENT APPLICATION NUMBER: US/09/951,845
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)...(517)
US-09-951-845-1
Query Match 59.6%; Score 201; DB 10; Length 523;
Best Local Similarity 100.0%; Pred. No. 8.5e-50;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 GGTTCGGGAGCAGCTTCCCGTCTCAGAGGGGCTGAAAATGTCTCTCCGAGATCC 196
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Db 517 GGTTCGGGAGCAGCTTCCCGTCTCAGAGGGGCTGAAAATGTCTCTCTCCGAGATCC 458
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QY 197 CTTGGCGTGCACCAATTCCTTAATCTTCAGGCGCTCCCGTGTGCTACAGATTTCCT 256  
 Db 457 CTTGGCGTGCACCAATTCCTTAATCTTCAGGCGCTCCCGTGTGCTACAGATTTCCT 398  
 QY 257 ACCCAAGCTTTCCCATGTGGAGCAGCCGCCCATGTGCTGCTTTTGCAGTAAAGAT 316  
 Db 397 ACCCAAGCTTTCCCATGTGGAGCAGCCGCCCATGTGCTGCTTTTGCAGTAAAGAT 338  
 QY 317 GTAGTGTGCTCCTCTGGGCGAG 337  
 Db 337 GTAGTGTGCTCCTCTGGGCGAG 317

RESULT 6  
 US-09-374-671-1/c  
 ; Sequence 1, Application US/09374671  
 ; Patent No. US2002012963A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morgenstern, Jay P.  
 ; APPLICANT: Kanieczny, Andrzej  
 ; APPLICANT: Bizindaukas, Christine B.  
 ; APPLICANT: Brauer, Andrew W.  
 ; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 ; TITLE OF INVENTION: Dander and Uses Therefor  
 ; NUMBER OF SEQUENCES: 104  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/374,671  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/491,861  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mandragoras, Amy E.  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 742-4214  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 525 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..525  
 ; FEATURE:  
 ; NAME/KEY: mat\_peptide  
 ; LOCATION: 79..525  
 ; US-09-374-671-1  
 Query Match 21.8%; Score 73.4; DB 10; Length 525;  
 Best Local Similarity 64.6%; Pred. No. 2.2e-12;  
 Matches 126; Conservative 0; Mismatches 66; Indels 3; Gaps 1;  
 QY 140 TTCGGAAACGAGCTCCCTGTCGAGGCGTGAATGCTCTCTCCGAGAGTCCCTT 199

Db 516 TCCTGGAGAGCAGGTTTCGCTGCGGAGTTCCTCCAAATCTCTCTGTTTC---AATCCTTT 460  
 QY 200 GCGCTGCACCAATTCCTTAATCTTCAGGCGCTCCCGTGTGCTACAGATTTCCTACC 259  
 Db 459 GCGCTGCAGAAATTCCTCCGAAATCTCTCCAGGCTCTTGGCTGCTGCTCAGGATCCCTCC 400  
 QY 260 CACAAGCTTTCCCATGTGGAGCAGCCGCCCATGTGCTGCTTTTGCAGTAAAGATGA 319  
 Db 399 CAGAGCTTGGCATTCGGATCTGCTCCCATGAGGCTCGCCCTCGCAGTAGAGAATGA 340  
 QY 320 GTGCTCCTCTCTGGG 334  
 Db 339 GTGCTCCTCTACCGG 325

RESULT 7  
 US-09-854-847-25/c  
 ; Sequence 25, Application US/09854847  
 ; Patent No. US20020107375A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mathur, Brian  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; TITLE OF INVENTION: No. US20020107375A1 Human Lipocalin Homologs and Polynucleot  
 ; FILE REFERENCE: LEX-0173-USA  
 ; CURRENT APPLICATION NUMBER: US/09/854,847  
 ; CURRENT FILING DATE: 2001-09-10  
 ; PRIOR APPLICATION NUMBER: US 60/203,874  
 ; PRIOR FILING DATE: 2000-05-12  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 25  
 ; LENGTH: 432  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-854-847-25  
 Query Match 13.2%; Score 44.6; DB 10; Length 432;  
 Best Local Similarity 51.8%; Pred. No. 0.00057;  
 Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;  
 QY 123 CCGGGGCTGCTAGTGTTCGGGAACGAGCTTCCTGCTGCGAGGCGGTGCAATATGTC 182  
 Db 431 CAGGGCGCTCTCTCTCTCAGAGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372  
 QY 183 TCTTCCGAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242  
 Db 371 TCTTCCGAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312  
 QY 243 GTATCAGAAATTCCTCCCAAGCTTCCCATGTGGAGCAGGCGCCCATGTGCTGCTGCT 302  
 Db 311 ACATCTGGTCTCGGCTGTAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252  
 QY 303 TTGCACTAAAGAGT 317  
 Db 251 TAGATGTAAGAGGAGC 237

RESULT 8  
 US-10-143-576-1/c  
 ; Sequence 1, Application US/10143576  
 ; Publication No. US2003001351A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HU, Song et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
 ; TITLE OF INVENTION: USES THEREOF  
 ; FILE REFERENCE: C1001237  
 ; CURRENT APPLICATION NUMBER: US/10/143,576  
 ; CURRENT FILING DATE: 2002-05-13  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 555

Mon Feb 10 11:11:52 2003

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-143-576-1

Query Match 13.2%; Score 44.6; DB 9; Length 555;
Best Local Similarity 51.8%; Pred. No. 0.00062;
Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 123 CCGGGGCTCCCTAGTGTGGGAACGACGCTTCCGCTGTGAGGGCGTGAATGTCC 182
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Db 554 CAGGGCGCTCCCTAGTGTGGGAACGACGCTTCCGCTGTGAGGGCGTGAATGTCC 182
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QY 183 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 242
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Db 494 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 242
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QY 243 GTATCAGAAATTCCTACCAACGCTTCCGCTGTGAGGGCGTGAATGTCC 302
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Db 434 ACATCTGGGTCCGCTGTGAGGGCGTGAATGTCC 375
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QY 303 TTGCAGTAAAGATG 317
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Db 374 TAGATGTAAGGAGG 360
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RESULT 9
US-09-854-847-1/c
; Sequence 1, Application US/09854847
; Patent No. US20020107375A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020107375A1 Human Lipocalin Homologs and Polynucleotide
; FILE REFERENCE: LEX-0173-USA
; CURRENT APPLICATION NUMBER: US/09/854.847
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 555
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-847-1

Query Match 13.2%; Score 44.6; DB 10; Length 555;
Best Local Similarity 51.8%; Pred. No. 0.00062;
Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 123 CCGGGGCTCCCTAGTGTGGGAACGACGCTTCCGCTGTGAGGGCGTGAATGTCC 182
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QY 183 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 242
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Db 494 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 242
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QY 243 GTATCAGAAATTCCTACCAACGCTTCCGCTGTGAGGGCGTGAATGTCC 302
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QY 303 TTGCAGTAAAGATG 317
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Db 374 TAGATGTAAGGAGG 360
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RESULT 10
US-09-800-729-37/c
; Sequence 37, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
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; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-37

Query Match 13.2%; Score 44.6; DB 10; Length 570;
Best Local Similarity 51.8%; Pred. No. 0.00063;
Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 123 CCGGGGCTCCCTAGTGTGGGAACGACGCTTCCGCTGTGAGGGCGTGAATGTCC 182
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 CAGGGCGCTCCCTAGTGTGGGAACGACGCTTCCGCTGTGAGGGCGTGAATGTCC 182
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QY 183 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 242
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Db 313 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 254
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 243 GTATCAGAAATTCCTACCAACGCTTCCGCTGTGAGGGCGTGAATGTCC 302
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 ACATCTGGGTCCGCTGTGAGGGCGTGAATGTCC 194
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QY 303 TTGCAGTAAAGATG 317
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Db 193 TAGATGTAAGGAGG 179
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RESULT 11
US-09-854-847-9/c
; Sequence 9, Application US/09854847
; Patent No. US20020107375A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020107375A1 Human Lipocalin Homologs and Polynucleotide
; FILE REFERENCE: LEX-0173-USA
; CURRENT APPLICATION NUMBER: US/09/854.847
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 579
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-847-9

Query Match 13.2%; Score 44.6; DB 10; Length 579;
Best Local Similarity 51.8%; Pred. No. 0.00063;
Matches 101; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 123 CCGGGGCTCCCTAGTGTGGGAACGACGCTTCCGCTGTGAGGGCGTGAATGTCC 182
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QY 183 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 242
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Db 518 TCCTCCGAGAGTCCCTTCCGCTGTGAGGGCGTGAATGTCC 259
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QY 243 GTATCAGAAATTCCTACCAACGCTTCCGCTGTGAGGGCGTGAATGTCC 302
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; PRIOR APPLICATION NUMBER: 60/069212  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069278  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069334  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069694  
; PRIOR FILING DATE: 1997-12-16  
; PRIOR APPLICATION NUMBER: 60/072320  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: 60/073612  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: 60/074086  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/074092  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-02-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081203  
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; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/086414  
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; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088730

; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088741  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088810  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088858  
; PRIOR FILING DATE: 1998-06-11  
; PRIOR APPLICATION NUMBER: 60/089532  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089599  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089907  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089947  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/090349  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: 60/090429  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090445  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090538  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090863  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07

Query Match 12.98; Score 43; Ds 9; Length 762;  
Best Local Similarity 51.38; Pred No. 0.0021;  
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;  
QY 123 CCGGGGGTGGCTAGTGTGCGGAGACGAGCTTCCGCTGCGAGGGCGGTGAAGTGC 182  
DB 579 CAGGGGGCTCCCTCTGCTCAGGTTGCATGCTGCTGGGGCAGCATGACCATG 520  
QY 183 TCTTCGAGAGTCCCTTCCGCTGCGACCAATTTCTTCCAGGGCTTCCCGTTG 242  
DB 519 TCCTTGGGGAGCCCGAGGGTCCGGGTAGAGTCTCTGGAAGGACTTCAGAGCTTGGGACTC 460  
QY 243 GTATCGAATTTCTACCCACAGCTTCCCATGTGGAGCAGGCCCCCATGTGGTGTCT 302  
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QY 303 TTGCAATAAGATG 317  
DB 399 TAGATGTAAGAGAG 385

RESULT 14  
US-10-121-049-237/c  
; Sequence 237, Application US/10121049  
; Publication No. US2003002239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K

Mon Feb 10 11:11:52 2003

us-09-099-823-3.rnpb

Page 8

```

1 APPLICANT: Wong, William
2 APPLICANT: Zhang, Zemin
3 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
4 TITLE OF INVENTION: ACIDS ENCODING THE SAME
5 FILE REFERENCE: P33303C17
6 CURRENT APPLICATION NUMBER: US/10/121,049
7 CURRENT FILING DATE: 2002-04-12
8
9 Prior Application removed - See File Wrapper or Palm
10
11 NUMBER OF SEQ ID NOS: 550
12
13 SEQ ID NO 237
14 LENGTH: 762
15 TYPE: DNA
16 ORGANISM: Homo Sapien
17
18 US-10-121-049-237

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Query Match 12.8%; Score 43; DB 9; Length 762;  
Best Local Similarity 51.3%; Pred. No. 0.0021;  
Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

[illegible]

RESULT 15

US-10-123-904-237/c

; Sequence 237, Application US/10123904

; Publication No. US2003002328A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gottslien, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Genlin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330RIC54

; CURRENT APPLICATION NUMBER: US/10/123,904

; CURRENT FILING DATE: 2002-04-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 237

; LENGTH: 762

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-123-904-237

Query Match 12.8%; Score 43; DB 9; Length 762;  
Best Local Similarity 51.3%; Pred. No. 0.0021;

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 Matches 100; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 123 CCGGGGCTCTAGTGTTCGGAGACAGCTTCCTCTGTCAGGGGCTGAATATCC 182
Db 579 CAGGGCCCTCTTCTCTCAGGTTGATGCACTGACGGGACATGACCATCATG 520
QY 183 TCTCCGAGAGTCCTTCGGCTGTCACCAATTTCTTAATTTCTCCAGGGCTTCGGGTG 242
Db 519 TCTTTGGGAGCCCCAGGTCGGGTAGAGTCTCTGGAGAGATCTCAGAGCTGGGGACTC 460
QY 243 GATACAGATTCCTACCCACAGCTTTCCATGTGGGAGCAGGCCCCCATGTGTCGTCT 302
Db 459 ACATCTCTGGTCCGCTGTGTAGAGCTGCACCATGTCGAGGGCCCCCTCCAGTCTCTTG 400
QY 303 TTGCAGTAAAGATG 317
Db 399 TAGATGTAAAGAGC 385

Search completed: February 9, 2003, 22:08:26
Job time : 33.9802 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:05:30 ; Search time 936.771 Seconds  
(without alignments)  
5826.269 Million cell updates/sec

Title: US-09-099-823-3

Perfect score: 337

Sequence: 1 GGGGAGAGAGACTTTATTT.....TAGTGTGCTCTCTGGGAG 337

Scoring table: IDENTITY\_NTC

Gap: 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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| 5:  | em_estov.*    |
| 6:  | em_estpl.*    |
| 7:  | em_estro.*    |
| 8:  | em_htc.*      |
| 9:  | gb_estl.*     |
| 10: | gb_est2.*     |
| 11: | gb_htc.*      |
| 12: | gb_est3.*     |
| 13: | gb_est4.*     |
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| 15: | em_estfun.*   |
| 16: | em_estom.*    |
| 17: | gb_gss.*      |
| 18: | em_gss_hum.*  |
| 19: | em_gss_inv.*  |
| 20: | em_gss_pln.*  |
| 21: | em_gss_vrt.*  |
| 22: | em_gss_fun.*  |
| 23: | em_gss_mam.*  |
| 24: | em_gss_mus.*  |
| 25: | em_gss_othe.* |
| 26: | em_gss_pro.*  |
| 27: | em_gss_rod.*  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
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| 2          | 335.4 | 99.5        | 477    | 9 AI251747  | AI251747 qh90f12.x |
| 3          | 335   | 99.4        | 415    | 9 AA460385  | AA460385 zx51e06.r |
| 4          | 335   | 99.4        | 532    | 10 AW513637 | AW513637 x047h10.x |
| 5          | 333.8 | 99.1        | 513    | 9 AA977608  | AA977608 on61e03.s |
| 6          | 328.8 | 97.6        | 349    | 9 AI143970  | AI143970 qe01c11.x |

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| 9  | 79    | 23.4 | 501  | 10 | AW049121 |
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| 14 | 53.8  | 16.0 | 312  | 9  | AA851021 |
| 15 | 51    | 15.1 | 322  | 12 | BA288401 |
| 16 | 48    | 14.2 | 494  | 14 | BA7029   |
| 17 | 46.6  | 13.8 | 1020 | 17 | CNS03858 |
| 18 | 45.8  | 13.6 | 758  | 17 | BH35934  |
| 19 | 45    | 13.4 | 742  | 13 | BI520644 |
| 20 | 44.2  | 13.1 | 417  | 14 | N68123   |
| 21 | 44    | 13.1 | 454  | 12 | BF405590 |
| 22 | 44    | 13.1 | 850  | 13 | BI603359 |
| 23 | 43.4  | 12.9 | 494  | 14 | BQ32434  |
| 24 | 43    | 12.8 | 452  | 10 | AW009446 |
| 25 | 43    | 12.8 | 910  | 17 | CNS00600 |
| 26 | 43    | 12.8 | 1139 | 14 | BQ435429 |
| 27 | 42.8  | 12.7 | 513  | 12 | BF403655 |
| 28 | 42.8  | 12.7 | 825  | 13 | BI956738 |
| 29 | 42.4  | 12.6 | 480  | 9  | AI840309 |
| 30 | 42.2  | 12.5 | 1101 | 17 | CNS00600 |
| 31 | 41.8  | 12.4 | 506  | 9  | AI854266 |
| 32 | 41.8  | 12.4 | 733  | 17 | AG167844 |
| 33 | 41.8  | 12.4 | 799  | 12 | BG446253 |
| 34 | 41.6  | 12.3 | 933  | 13 | BI553344 |
| 35 | 41.6  | 12.3 | 1051 | 12 | BG025592 |
| 36 | 41.4  | 12.3 | 674  | 17 | BI9096   |
| 37 | 41.2  | 12.2 | 1025 | 17 | CNS031NW |
| 38 | 41    | 12.2 | 881  | 13 | BI522969 |
| 39 | 40.8  | 12.1 | 308  | 9  | AI836992 |
| 40 | 40.8  | 12.1 | 797  | 14 | AG721811 |
| 41 | 40.8  | 12.1 | 833  | 17 | AG748616 |
| 42 | 40.8  | 12.1 | 909  | 17 | CNS0037L |
| 43 | 40.8  | 12.1 | 1077 | 17 | CNS0156Q |
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| 45 | 40.6  | 12.0 | 1104 | 17 | CNS076QT |

## ALIGNMENTS

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LOCUS

DEFINITION

AA460323

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

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zx51e06.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:795778  
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EST.  
human.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 337)  
Hillier, L., Allen, M., Bowles, L., Dubucque, T., Geisel, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, P.,  
Schallerberg, K., Steptoe, M., Tan, F., Theisling, B., White, J., Wyllie,  
T., Waterston, R., and Wilson, R.  
WashU-Nerck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand







PROTEIN. ; mRNA sequence.  
AA977608.1 GI:3155054  
EST.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 513)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](http://info@image.llnl.gov)) for further information.  
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High quality sequence stop. 339.  
Location/Qualifiers  
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/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
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Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung MHL19W, testis NHT, and B-cell  
NCI CGAP GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo.  
88 a 133 c 158 g 134 t

BASE COUNT 88 a 133 c 158 g 134 t

ORIGIN  
Query Match 99.1%; Score 333.8; DB 9; Length 513;  
Best Local Similarity 99.4%; Pred. No. 8e-80; Indels 0; Gaps 0;  
Matches 335; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGAGGACTTTATTGGAGTCAGGTGGGAGCAGGAGGAGGTCATGGCTGGA 60  
DB 12 GGGGAGAGGACTTTATTGGAGTCAGGTGGGAGCAGGAGGAGGTCATGGCTGGA 71  
QY 61 GGGTAGGTCCAGGTGGTCCAGGCTCTGTCTGGTGGTGGTGGGCTCTGGAGGTGCAG 120  
DB 72 GGGTAGGTCCAGGTGGTCCAGGCTCTGTCTGGTGGTGGTGGGCTCTGGAGGTGCAG 131  
QY 121 ACCCGGGGCTGCTAGTGTTCGGGAACGACGCTCCGCTCTCGAGGGGCTGAAATGT 180  
DB 132 ACCCGGGGCTGCTAGTGTTCGGGAACGACGCTCCGCTCTCGAGGGGCTGAAATGT 191  
QY 181 CTCTCTCCGAGAGTCCCTGCGCTGCACCAATTTCTTAATTTCTCCAGGCTCCCGGT 240  
DB 192 CTCTCTCCGAGAGTCCCTGCGCTGCACCAATTTCTTAATTTCTCCAGGCTCCCGGT 251  
QY 241 TGGTATCAGAAATCTTACCAACAAGCTTTCCATGTGGAGCAGGCCGCCATGGTGTGTGT 300  
DB 252 TGGTATCAGAAATCTTACCAACAAGCTTTCCATGTGGAGCAGGCCGCCATGGTGTGTGT 311  
QY 301 CTTTGCAGTAAAGATAGTGTGCTCCCTCTCGGCGAG 337  
DB 312 CTTTGCAGTAAAGATAGTGTGCTCCCTCTCGGCGAG 348

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3' similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. ; mRNA  
sequence.  
A1143970  
VERSION A1143970.1 GI:3665779  
KEYWORDS EST  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 349)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: 40m13 fwd. ET from Amersham.  
Location/Qualifiers  
1. 349  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:1737716"  
/clone\_lib="Soares\_testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGGCCGCCAATTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 55 a 80 c 115 g 99 t

ORIGIN  
Query Match 97.6%; Score 328.8; DB 9; Length 349;  
Best Local Similarity 99.4%; Pred. No. 1.7e-78; Indels 0; Gaps 0;  
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGAGAGGACTTTATTGGAGTCAGGTGGGAGCAGGAGGAGGTCATGGCTGGA 60  
DB 18 GGGGAGAGGACTTTATTGGAGTCAGGTGGGAGCAGGAGGAGGTCATGGCTGGA 77  
QY 61 GGGTAGGTCCAGGTGGTCCAGGCTCTGTCTGGTGGTGGTGGGCTCTGGAGGTGCAG 120  
DB 78 GGGTAGGTCCAGGTGGTCCAGGCTCTGTCTGGTGGTGGTGGGCTCTGGAGGTGCAG 137  
QY 121 ACCCGGGGCTGCTAGTGTTCGGGAACGACGCTCCGCTCTCGAGGGGCTGAAATGT 180  
DB 138 ACCCGGGGCTGCTAGTGTTCGGGAACGACGCTCCGCTCTCGAGGGGCTGAAATGT 197  
QY 181 CTCTCTCCGAGAGTCCCTGCGCTGCACCAATTTCTTAATTTCTCCAGGCTCCCGGT 240  
DB 198 CTCTCTCCGAGAGTCCCTGCGCTGCACCAATTTCTTAATTTCTCCAGGCTCCCGGT 257  
QY 241 TGGTATCAGAAATCTTACCAACAAGCTTTCCATGTGGAGCAGGCCGCCATGGTGTGTGT 300  
DB 258 TGGTATCAGAAATCTTACCAACAAGCTTTCCATGTGGAGCAGGCCGCCATGGTGTGTGT 317  
QY 301 CTTTGCAGTAAAGATAGTGTGCTCCCTCTCGGCGAG 332

FEATURES  
source  
1. 349  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:1737716"  
/clone\_lib="Soares\_testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGGCCGCCAATTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

us-09-099-823-3.rst

Mon Feb 10 11:11:55 2003

```

; QY 301 CTTTCAGTAAGAAGTAGTGGTCCCTCCTGGCGAG 337
; ||||| ||||| ||||| ||||| ||||| |||||
; Db 304 CTTTCAGTAAGAAGTAGTGGTCCCTCCTGGCGAG 340

RESULT 8
! AA936288 431 bp mRNA linear EST 29-APR-1998
LOCUS on75f11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1562541 3' similar to TR:Q63613 Q63613 ODORANT-BINDING
PROTEIN. ; mRNA sequence.
AA936288
VERSION AA936288.1 GI:3094206
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 431)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. EF from Amersham
High quality sequence stop: 344.
Location/Qualifiers
FEATURES
source
1..431
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1562541"
/lab.host="Soares_NFL_T_GBC_S1"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site: 1: Not I; Site: 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 73 a 111 c 136 g 110 t
ORIGIN
Query Match 85.0%; Score 286.4; DB 9; Length 431;
Best Local Similarity 94.4%; Pred. No. 4.9e-67; Indels 2; Gaps 2;
Matches 318; Conservative 0; Mismatches 17;

QY 1 GGGGAGAGAGCTTTATTTGGAGTCAGGTGGGTGGGAGGAGGATGATGCTGGA 60
Db 4 GGGGAGAGAGCTTTATTTGGAGTCAGGTGGGTGGGAGGAGGATGATGCTGGA 63
QY 61 GGGTAGTCCAGGTGGTCCGGGCTCTGTCGTGTTAGTGGGTGGGTCTGGAGGTGCAG 120
Db 64 GGGTAGTCCAGGTGGTCCGGGCTCTGTCGTGTTAGTGGGTGGGTCTGGAGGTGCAG 123
QY 121 ACCGGGGGCTGCTAGTGTTCGGGAACGACCTTCCTGCTGCGGGGCTGAAATGT 180
Db 124 ACCGGGGGCTGCTAGTGTTCGGGAACGACCTTCCTGCTGCGGGGCTGAAATGT 183
QY 181 CTTCTCCGAGAGTCCCTTGTGCTGCACCAATTTCTTAATTTCTTCAGGGCTCCCGGT 240
Db 184 CTTCTCCGAGAGTCCCTTGTGCTGCACCAATTTCTTAATTTCTTCAGGGCTCCCGGT 243
QY 241 TGGTATCAGATTCCTACCCACAAGCTTTCCCATGTGGAGAGGCCCCCATGCTGTTGT 300

; QY 301 CTTTCAGTAAGAAGTAGTGGTCCCTCCTGGCGAG 337
; ||||| ||||| ||||| ||||| ||||| |||||
; Db 304 CTTTCAGTAAGAAGTAGTGGTCCCTCCTGGCGAG 340

RESULT 7
! AI219510 499 bp mRNA linear EST 30-NOV-1998
LOCUS qh24q02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1845603 3' similar to TR:Q63613 Q63613 ODORANT-BINDING
PROTEIN. ; mRNA sequence.
AI219510
VERSION AI219510.1 GI:3801713
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 499)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 536 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 330.
Location/Qualifiers
FEATURES
source
1..499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1845603"
/lab.host="Soares_NFL_T_GBC_S1"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site: 1: Not I; Site: 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 85 a 135 c 151 g 126 t
ORIGIN
Query Match 92.4%; Score 311.4; DB 9; Length 499;
Best Local Similarity 95.3%; Pred. No. 9e-74; Indels 0; Gaps 0;
Matches 321; Conservative 0; Mismatches 16;

QY 1 GGGGAGAGAGCTTTATTTGGAGTCAGGTGGGTGGGAGGAGGATGATGCTGGA 60
Db 4 GGGGAGAGAGCTTTATTTGGAGTCAGGTGGGTGGGAGGAGGATGATGCTGGA 63
QY 61 GGGTAGTCCAGGTGGTCCGGGCTCTGTCGTGTTAGTGGGTGGGTCTGGAGGTGCAG 120
Db 64 GGGTAGTCCAGGTGGTCCGGGCTCTGTCGTGTTAGTGGGTGGGTCTGGAGGTGCAG 123
QY 121 ACCGGGGGCTGCTAGTGTTCGGGAACGACCTTCCTGCTGCGGGGCTGAAATGT 180
Db 124 ACCGGGGGCTGCTAGTGTTCGGGAACGACCTTCCTGCTGCGGGGCTGAAATGT 183
QY 181 CTTCTCCGAGAGTCCCTTGTGCTGCACCAATTTCTTAATTTCTTCAGGGCTCCCGGT 240
Db 184 CTTCTCCGAGAGTCCCTTGTGCTGCACCAATTTCTTAATTTCTTCAGGGCTCCCGGT 243
QY 241 TGGTATCAGATTCCTACCCACAAGCTTTCCCATGTGGAGAGGCCCCCATGCTGTTGT 300
Db 244 TGGTATCAGATTCCTACCCACAAGCTTTCCCATGTGGAGAGGCCCCCATGCTGTTGT 303

```



| RESULT 11 | BB618259/c | BB618259 | 603 bp | mRNA | linear | EST 26-OCT-2001 |
|-----------|------------|----------|--------|------|--------|-----------------|
| LOCUS     |            |          |        |      |        |                 |

FEATURES

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATTCGATATTAATATCCGCCGCCGCC vector]. cDNA was cloned into the XhoI and BamHI sites of a modified pluescript kist k(+) after BamHI digestion from Lambda FLC 1. Cloning sites, 5' end: SalI, 3' end: BamHI.

|                       | 168 a                 | 131 c                    | 167 g               | 137 t       |         |
|-----------------------|-----------------------|--------------------------|---------------------|-------------|---------|
| Query Match           | 21.5%                 | Score 72.6;              | DB 10;              | Length 603; |         |
| Best Local Similarity | 63.4%;                | Pred. No. 2.9e-09;       |                     |             |         |
| Matches 144;          | Conservative          | 0;                       | Mismatches 79;      | Indels 4;   | Gaps 2; |
| 107                   | CTCTGGAGTGCAGAGCCCGSG | -GCTCGCTAGTGTTCGGGACGAGC | GTTCGCGTCTGCA       | 165         |         |
| 503                   | CTACAGCTGTTCGAGNCTGG  | GTAGTCTGCTTTCACACATTTT   | CTCGATCT            | 544         |         |
| 166                   | GGGGCGGTGAATGTCCTCCG  | AGAGTCCCTTCGCGTCACCAATTT | CTTCAAAATCTT        | 225         |         |
| 543                   | CTGCACAAACATGTTTCCAG  | TCCGAGATTCATGCGCTTT      | TATGAATCTTCAAAATCTT | 484         |         |
| 226                   | CTAGGGCTCCCGGTGGTATCA | GAATCTCTACCCACAGCTTT     | TCCCATGTGA          | --GCA 282   |         |
| 483                   | CTATGGCCCTCGATTTTCAG  | AGATCTCCCATGAGCTTT       | TCCCATCGAATGAGC     | 424         |         |
| 283                   | GGCCGCCAGTGGTGTCTTTG  | CAGTAAAAGATGTAGTGTG      | CTGCTC              | 329         |         |
| 423                   | ACCTGCTGCTTCTGCTGCTT  | CTGCTGCTGCTGCTGCTG       | CTGCTGCTGCTGCTGCTG  | 377         |         |

| BASE COUNT                                                                                                                                                                                                                                                                                                                                                                                                                                         | 169 a                                                                                                                                | 153 c                   | 148 g                                     | 124 t | Xho1; Estimated insert size approx.1 kb* |  |  |  |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|-------------------------|-------------------------------------------|-------|------------------------------------------|--|--|--|
| ORIGIN                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| Query Match                                                                                                                                                                                                                                                                                                                                                                                                                                        | 20.9%; Score 70.4; DB 10; Length 594;                                                                                                |                         |                                           |       |                                          |  |  |  |
| Best Local Similarity                                                                                                                                                                                                                                                                                                                                                                                                                              | 60.4%; Pred. No.1.le-08;                                                                                                             |                         |                                           |       |                                          |  |  |  |
| Matches 116; Conservative                                                                                                                                                                                                                                                                                                                                                                                                                          | 0; Mismatches 76; Indels 0; Gaps 0;                                                                                                  |                         |                                           |       |                                          |  |  |  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 135                                                                                                                                  | TAGTGTTCGGGAAGCAGCAGTTC | CGCGTCGACGAGGGGCGGAANAATGCTCCTCCGAGAGT    | 194   |                                          |  |  |  |
| DB                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 539                                                                                                                                  | ATGCTTCCTAGAGGCAATGTTT  | TCACCTGCTTGGGATGAGATGTTGCTGGGTTGAG        | 480   |                                          |  |  |  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 195                                                                                                                                  | CCCTGTGGCTGCACCAATTTCT  | TAATCTTCCAGGCGCTCCGCGTGTGATACAGAAATTC     | 254   |                                          |  |  |  |
| DB                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 479                                                                                                                                  | CCTCCAGCTCTTACAGCAATCT  | CGAAATCTTCCAGGCGCTCCGCGTGTGATACAGAAATTC   | 420   |                                          |  |  |  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 255                                                                                                                                  | CTACCCACAGCTTTCACATCTG  | GAGCAGCGCCCGCATGCTGCTGCTTCACGATAAAG       | 314   |                                          |  |  |  |
| DB                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 419                                                                                                                                  | CTGCCACAGCTTTCACATCTG   | GAATTTGGAATGATGCTGCTGATTTTGGCTCATAGTAGAAG | 360   |                                          |  |  |  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 315                                                                                                                                  | ATGTAGTGGTCC            | 326                                       |       |                                          |  |  |  |
| DB                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 359                                                                                                                                  | ATATAGTGGTCC            | 348                                       |       |                                          |  |  |  |
| RESULT 13                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| LOCUS                                                                                                                                                                                                                                                                                                                                                                                                                                              | A1877465/c                                                                                                                           |                         |                                           |       | 519 bp mRNA linear EST 21-JUL-1999       |  |  |  |
| DEFINITION                                                                                                                                                                                                                                                                                                                                                                                                                                         | u010609_r1 Soares_NMPu Mus musculus cDNA clone IMAGE:1434737 5', similar to IR:063613 063613 ODORANT-BINDING PROTEIN. ;, mRNA        |                         |                                           |       |                                          |  |  |  |
| ACCESSION                                                                                                                                                                                                                                                                                                                                                                                                                                          | A1877465                                                                                                                             |                         |                                           |       |                                          |  |  |  |
| VERSION                                                                                                                                                                                                                                                                                                                                                                                                                                            | A1877465                                                                                                                             |                         |                                           |       |                                          |  |  |  |
| KEYWORDS                                                                                                                                                                                                                                                                                                                                                                                                                                           | EST.                                                                                                                                 |                         |                                           |       |                                          |  |  |  |
| SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                             | house mouse.                                                                                                                         |                         |                                           |       |                                          |  |  |  |
| ORGANISM                                                                                                                                                                                                                                                                                                                                                                                                                                           | Mus musculus                                                                                                                         |                         |                                           |       |                                          |  |  |  |
| REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. |                         |                                           |       |                                          |  |  |  |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1 (bases 1 to 519)                                                                                                                   |                         |                                           |       |                                          |  |  |  |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                              | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.                                                                                        |                         |                                           |       |                                          |  |  |  |
| COMMENT                                                                                                                                                                                                                                                                                                                                                                                                                                            | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index                                                    |                         |                                           |       |                                          |  |  |  |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                                            | Unpublished (1997)                                                                                                                   |                         |                                           |       |                                          |  |  |  |
| CONTACT                                                                                                                                                                                                                                                                                                                                                                                                                                            | Contact: Robert Strausberg, Ph.D.                                                                                                    |                         |                                           |       |                                          |  |  |  |
| EMAIL                                                                                                                                                                                                                                                                                                                                                                                                                                              | Email: cgap@femail.nih.gov                                                                                                           |                         |                                           |       |                                          |  |  |  |
| THIS CLONE IS AVAILABLE                                                                                                                                                                                                                                                                                                                                                                                                                            | royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.                                |                         |                                           |       |                                          |  |  |  |
| MG1:918805                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| Putative full length read                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| vector to vector length is                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| Seq primer: -28ml3 rev2                                                                                                                                                                                                                                                                                                                                                                                                                            | BT from Amersham                                                                                                                     |                         |                                           |       |                                          |  |  |  |
| High quality sequence stop:                                                                                                                                                                                                                                                                                                                                                                                                                        | 503.                                                                                                                                 |                         |                                           |       |                                          |  |  |  |
| FEATURES                                                                                                                                                                                                                                                                                                                                                                                                                                           | Location/Qualifiers                                                                                                                  |                         |                                           |       |                                          |  |  |  |
| SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1..519                                                                                                                               |                         |                                           |       |                                          |  |  |  |
| /organism="Mus musculus"                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /db_xref="taxon:10090"                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /clone="IMAGE:1434737"                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /clone.lib="Soares_NMPu"                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /sex="female"                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /dev_stage="adult"                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /lab_host="DH10B"                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| /note="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia) digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| BASE COUNT                                                                                                                                                                                                                                                                                                                                                                                                                                         | 148 a                                                                                                                                | 112 c                   | 142 g                                     | 116 t | 1 others                                 |  |  |  |
| ORIGIN                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                      |                         |                                           |       |                                          |  |  |  |
| Query Match                                                                                                                                                                                                                                                                                                                                                                                                                                        | 19.2%; Score 64.8; DB 9; Length 519;                                                                                                 |                         |                                           |       |                                          |  |  |  |

us-09-099-823-3.rst

Mon Feb 10 11:11:55 2003

Best Local Similarity 66.1%; Pred. No. 3.6e-07;  
Matches 109; Conservative 0; Mismatches 53; Indels 3; Gaps 1;  
QY 168 GCGGTGAATGTCCTCCGAGAGTCCCTGGCGTGCACCAATTTCTTAAATTTCTCC 227  
Db 514 GGCACACATGTTTTCAGTCGGAGATTCAGCGCTTATGAAATTTCTTAAATTTCTCC 455  
QY 228 AGGCGTCCGGTGGTATCAGATTCACCCACAGCTTCCCATGGGA--GCAGG 284  
Db 454 ATGGCCCTGGAATTTACACAGAGTCTCCCATGAGCTTTCCCATCCGATGACGAC 395  
QY 285 CCCCCATGGTGTCTTTTGCAGTAAAGATGATGTGTCCTC 329  
Db 394 GTCCCATGTGCGCGCTTCGAGTAGAATGATGTGCTCATTC 350  
RESULT 14  
AA851021 312 bp mRNA linear EST 30-APR-1998  
LOCUS  
DEFINITION  
ESV163789 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone  
K01964 3' end, mRNA sequence.  
ACCESSION  
AA851021  
VERSION  
AA851021.1 GI:2938561  
KEYWORDS  
EST.  
SOURCE  
Rattus sp.  
ORGANISM  
Rattus sp.  
REFERENCE  
1 (Bases 1 to 312)  
Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J.,  
Kerlavage, A.R., and Adams, M.D.  
Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat  
Gene Index  
Unpublished (1998)  
CONTACT: Lee, NH  
The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
Seq primer: M13-21.  
Location/Qualifiers  
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/organism="Rattus sp."  
/db\_xref="ATCC (Inhost):2009422"  
/db\_xref="taxon:10118"  
/clone="K01964"  
/clone\_lib="Normalized rat ovary, Bento Soares"  
/note="Organ: ovary; Vector: pT3Pac; Site\_1: EcoRI;  
Site\_2: NotI"  
BASE COUNT 74 a 63 c 96 g 79 t  
ORIGIN  
Query Match 16.0%; Score 53.8; DB 9; Length 312;  
Best Local Similarity 63.6%; Pred. No. 0.00031;  
Matches 82; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
QY 149 GCAGTTCCTCCGTCGAGGCGTGAATGTCTCTCCGAGTCCCTTCGCGTGCAC 208  
Db 184 GCGTTCCTCCGTCGAGGCGTGAATGTCTCTCCGAGTCCCTTCGCGTGCAC 243  
QY 209 CAATTTCTTAAATTTCTCCAGGCTCCCGGTTGGTATCAGATTTCTTACCCACAGCTT 268  
Db 244 AGCATTTCTGAAATTTCTCCAGGCGCTTCGTTGATCCAGGGTTCTGCGCCACGAGTT 303  
QY 269 TCCCATGTG 277  
Db 304 TGCATTTGG 312  
RESULT 15  
BF288401

LOCUS  
DEFINITION  
BF288401 322 bp mRNA linear EST 28-NOV-2000  
Rattus norvegicus cDNA clone RIGT39 3' sequence, mRNA sequence.  
ACCESSION  
BF288401  
VERSION  
BF288401.1 GI:11219471  
KEYWORDS  
EST.  
SOURCE  
Norway rat.  
ORGANISM  
Rattus norvegicus  
REFERENCE  
1 (Bases 1 to 322)  
Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G.,  
Sultana, R., Tsai, J., White, J., Quackenbush, J., and Lee, N.H.  
Generation of ESTs from Normalized Rat Embryo, Bento Soares  
Unpublished (2000)  
Other ESTs: EST351585  
CONTACT: Lee, NH  
The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
This clone is available through the ATCC, contact the ATCC  
tel#703-365-2700 for further information.  
Location/Qualifiers  
i. 322  
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QY 209 CAATTTCTTAAATTTCTCCAGGCTCCCGGTTGGTATCAGATTTCTTACCCACAGCTT 268  
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QY 269 TCCCATGTGGA 279  
Db 305 TGCATTTGGGA 315  
Search completed: February 10, 2003, 04:58:18  
Job time : 947.771 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: February 9, 2003, 22:02:40 : Search time 2254.33 Seconds  
(without alignments)  
8933.518 Million cell updates/sec

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Perfect score: 692  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 6: gb.pat.\*
- 7: gb.pl.\*
- 8: gb.pr.\*
- 9: gb.ro.\*
- 10: gb.sts.\*
- 11: gb.sy.\*
- 12: gb.un.\*
- 13: gb.vi.\*
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- 41: em.hugo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | AX454620 | 688.8 | 99.5  | 739    | 6  | AX454620   | AX454620 Sequence  |
| 3          | AX454620 | 676   | 97.7  | 676    | 6  | AX083544   | AX083544 Sequence  |
| 4          | AX454620 | 676   | 97.7  | 676    | 6  | AX083544   | AX083544 Sequence  |
| 5          | AX454620 | 648.8 | 93.8  | 676    | 6  | AX083536   | AX083536 Sequence  |
| 6          | AX454620 | 648.8 | 93.8  | 676    | 6  | AX083536   | AX083536 Sequence  |
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| 11         | AX454620 | 560   | 80.9  | 782    | 6  | AX083546   | AX083546 Sequence  |
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ALIGNMENTS

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DEFINITION Sequence 205 from Patent WO0206284.  
ACCESSION AX454620  
VERSION AX454620.1 GI:21713934  
KEYWORDS human.  
SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS

Baker, K.P., Ferrara, N., Gerber, H., Gertsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.

**TITLE** Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
**JOURNAL** Patent: WO 020690-A 205 31-JAN-2002;  
 (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

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 Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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**VERSION** AX491098.1 GI:22323886  
**KEYWORDS**  
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**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
**TITLE** Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
**JOURNAL** Patent: WO 020690-A 205 03-JAN-2002;  
 Genentech, Inc. (US)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 676)  
 Pitiot,G., Lacazette,E. and Gachon,F.  
 Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 Patent: WO 0112806-A 9 22-FEB-2001;  
 Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)

JOURNAL Location/Qualifiers  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 676)  
 Lacazette,E., Gachon,A.M. and Pitiot,G.  
 A novel human odorant-binding protein gene family resulting from  
 genomic duplicons at 9q34: differential expression in the oral and  
 genital spheres  
 Hum. Mol. Genet. 9 (2), 289-301 (2000)

JOURNAL MEDLINE  
 PUBMED 10607840

REFERENCE 2 (bases 1 to 676)  
 Gachon,A.M.  
 Direct Submission  
 Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
 U884, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
 Dunant, Clermont Ferrand cedex01 63001, FRANCE

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Query Match 97.7%; Score 676; DB 9; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-143;  
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION  
 ACCESSION AJ251022  
 VERSION AJ251022.1 GI:6900068  
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 1 (bases 1 to 725)  
 Lacazette, E., Gachon, A.M. and Pitiot, G.  
 A novel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres  
 Hum. Mol. Genet. 9 (2), 289-301 (2000)  
 JOURNAL  
 MEDLINE 10607840  
 PUBMED 10607840  
 Gachon, A.M.  
 2 (bases 1 to 725)  
 Direct Submission  
 Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri Dunant, Clermont Ferrand cedex01 63001, FRANCE  
 JOURNAL  
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 LOCUS Sequence 5 from Patent WO0112806.  
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 ACCESSION AX083540.1 GI:13185350  
 VERSION  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 741)

AUTHORS Pitiot,G., Lacazette,E. and Gachon,F.  
 TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 JOURNAL Patent: WO 0112806-A 5 22-FEB-2001;  
 Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)  
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 Query Match 82.9%; Score 573.8; DB 6; Length 741;  
 Best Local Similarity 88.9%; Pred. No. 8.3e-120;  
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 Db 721 CCACCTGACTCCCAATAAAG 741  
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 LOCUS Homo sapiens mRNA for putative odorant binding protein ag (OBPIIa)  
 DEFINITION  
 HSA251024  
 ACCESSION AJ251024  
 VERSION AJ251024.1 GI:6900072  
 KEYWORDS OBPIIa gene; odorant binding protein.  
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 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 Lacazette,E., Gachon,A.M. and Pitiot,G.  
 1 (bases 1 to 741)  
 A novel human odorant-binding protein gene family resulting from  
 genomic duplicons at 9q34: differential expression in the oral and  
 genital spheres  
 Hum. Mol. Genet. 9 (2), 289-301 (2000)  
 JOURNAL MEDLINE 20076326  
 PUBMED 10607840  
 REFERENCE 2 (bases 1 to 741)  
 Gachon,A.M.  
 Direct Submission  
 Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
 U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
 Dunant, Clermont Ferrand cedex01 63001, FRANCE  
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 Query Match 82.9%; Score 573.8; DB 9; Length 741;  
 Best Local Similarity 88.9%; Pred. No. 8.3e-120;  
 Matches 659; Conservative 0; Mismatches 17; Indels 65; Gaps 1;  
 QY 3 CGCCAGTACCTCCGAGTCCGACACAGAGCTCTGGAGATGAAGACCTGTCTCTG 62  
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 DEFINITION Sequence 11 from Patent WO0112806.  
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 VERSION AX083546.1 GI:13185356  
 KEYWORDS  
 SOURCE human.  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Pitiot.G., Lacazette,B. and Gachon,F.  
 Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 Patent: WO 0112806-A 11 22-FEB-2001;  
 Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)  
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BASE COUNT 186 a 226 c 239 g 131 t  
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Query Match 80.9%; Score 560; DB 6; Length 782;  
 Best Local Similarity 86.4%; Pred. No. 1.1e-116;  
 Matches 676; Conservative 0; Mismatches 0; Indels 106; Gaps 1;

QY 3 CGCCAGTGCCTGCGAGGTGCGCAGACAGAGCTCTGAGATGAAGACCCCTGTTCTG 62  
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RESULT 12  
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 LOCUS  
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 ACCESSION AJ251027  
 VERSION AJ251027.1 GI:6900078  
 KEYWORDS OBPIIb gene; odorant binding protein.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 782)  
AUTHORS Lacazette, E., Gachon, A.M. and Piliot, G.  
TITLE A novel human odorant-binding protein gene family resulting from genomic duplications at 9q34: differential expression in the oral and genital spheres  
JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)  
MEDLINE 20076326  
PubMed 10607840  
REFERENCE 2 (bases 1 to 782)  
AUTHORS Gachon, A.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM U384, Universite d'Auvergne - Faculte de Medecine, 28, Place Henri Dunant, Clermont Ferrand cedex 01 63001, FRANCE  
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BASE COUNT 186 a 226 c 239 g 131 t  
ORIGIN

Query Match 80.9%; Score 560; DB 9; Length 782;  
Best Local Similarity 86.4%; Pred. No. 1.1e-116;  
Matches 676; Conservative 0; Mismatches 0; Indels 106; Gaps 1;

QY 3 CGCCAGTCACTCCGAGCTCGCAGACAGAGCTCTGGAGATGAGAGACCTGTCTTG 62  
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Db 781 AG 782

RESULT 13  
AR204078 LOCUS 522 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 1 from patent US 6365716.  
ACCESSION AR204078  
VERSION AR204078.1 GI:21500632  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 522)  
AUTHORS Conklin, D.C.  
TITLE Antibodies to lipocalin homologs  
JOURNAL Patent: US 6365716-A 1 02-APR-2002;  
FEATURES Location/Qualifiers  
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BASE COUNT 125 a 132 c 172 g 93 t  
ORIGIN

Query Match 74.3%; Score 514.4; DB 6; Length 522;  
Best Local Similarity 99.8%; Pred. No. 2.4e-106;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from Patent WO0223201.  
ACCESSION AX451327  
VERSION AX451327.1 GI:21698379  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1  
AUTHORS Lok S., Foster, D.C. and Holloway, J.L.  
TITLE Use of human pheromone polypeptides  
JOURNAL Patent: WO 0223201-A 1 21-MAR-2002;  
ZymoGenetics, Inc. (US)  
FEATURES  
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BASE COUNT 125 a 153 c 172 g 93 t  
ORIGIN  
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Best Local Similarity 99.8%; Pred. No. 2.4e-106;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 39 CTGGAGATGAAGACCTGTCTCTGGGTGTCACGCTCGCGCTGCGCGCTGCGCTGCTTC 98  
Db 2 CTCGAGATGAAGACCTGTCTCTGGGTGTCACGCTCGCGCTGCGCGCTGCGCTGCTTC 61  
QY 99 ACCCTGAGGAGGAGGATATCACAGGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAG 158  
Db 62 ACCCTGAGGAGGAGGATATCACAGGAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAG 121  
QY 159 GACTTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
Db 122 GACTTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181  
QY 219 GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278  
Db 182 GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241  
QY 279 ATCTGATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338  
Db 242 ATCTGATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301  
QY 339 ATGTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 398  
Db 302 ATGTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361  
QY 399 CATGGGGCCCTGCTCCATCGGAAGCTTGTGGTAGGAATCTGTATCAACCGGGAG 458

Db 362 CATGGGGCCCTGCTCCATCGGAAGCTTGTGGTAGGAATCTGTATCAACCGGGAG 421  
QY 459 GCCCTGGAAGAAATTTAGAAATTTGGTCAGCGCAAGGAGCTCTCGGAGGAGCAATTTTC 518  
Db 422 GCCCTGGAAGAAATTTAGAAATTTGGTCAGCGCAAGGAGCTCTCGGAGGAGCAATTTTC 481  
QY 519 ACGCCCTGCGAGAGGAGCTGCTGCCGAACAC 554  
Db 482 ACGCCCTGCGAGAGGAGCTGCTGCCGAACAC 517

RESULT 15  
AX083548  
LOCUS AX083548 542 bp DNA linear PAT 28-FEB-2001  
DEFINITION Sequence 13 from Patent WO0112B06.  
ACCESSION AX083548  
VERSION AX083548.1 GI:13185358  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 542)  
AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.  
TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
polypeptides and polynucleotides coding for said polypeptides and  
uses thereof  
JOURNAL Patent: WO 0112806-A 13 22-FEB-2001;  
Universite d'Auvergne (FR); Pitiot, Gilles (FR)  
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1..542  
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Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 249 ATGAGGAGGAGCTGCTGCTCCAGAGAAATCTGTATCGGAAGAGGAGGAGGAGGAGG 308  
Db 113 ATGAGGAGGAGCTGCTGCTCCAGAGAAATCTGTATCGGAAGAGGAGGAGGAGGAGG 172  
QY 309 AAATACAGCGCTATGCGGCGCAGAGAGCTCATCTACCTGACGAGCTCCCTCAGGAGGAG 368  
Db 173 AAATACAGCGCTATGCGGCGCAGAGAGCTCATATCTGACGAGGCTCCCTCAGGAGGAG 232  
QY 369 CACTACATCTTTTACTGCAAAAGACACGACCATGCGGCGCTGCTCCATCGGAAGAGCTT 428  
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QY 429 GTGGTAGGAATCTGTATCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 488  
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QY 489 CGCAAGGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 548  
Db 353 CGCAAGGAGCTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 412  
QY 549 GAACACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 608  
Db 413 GAACACTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 472  
QY 609 CCCGGACCACTGAGCTTACCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 668

Mon Feb 10 11:11:55 2003

us-09-099-823-4.rge

Page 11

Db 473 CCGGACCACTGGACTACCTCCAGCCATGACCTTCCTGCTCCACCCCACTGACT 532

Qy 669 CCATATATAG 678

Db 533 CCATATATAG 542

Search completed: February 10, 2003, 03:12:47  
Job time : 2260.33 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 19:57:40 ; Search time 254.241 Seconds  
(without alignments)  
6129.540 Million cell updates/sec

Title: US-09-099-823-4  
Perfect score: 692  
Sequence: 1 GAGCGCCAGTACCTGCGA.....ATTAAGTCCTTCTCCCCCA 692

Scoring table: IDENTITY\_NUC  
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Query Match | Length | ID  | Description                    |
|------------|-------------|--------|-----|--------------------------------|
| 1          | 692         | 100.0  | 692 | 20 AAX07456 Human BS124 specif |
| 2          | 692         | 100.0  | 692 | 20 AAX07456 Human BS124 specif |
| 3          | 690         | 99.7   | 690 | 21 AAZ91770 Human breast speci |
| 4          | 688.8       | 99.5   | 738 | 22 AAF54313 DNA encoding prote |
| 5          | 688.8       | 99.5   | 739 | 21 AAC58615 Human PRO1283 prot |
| 6          | 688.8       | 99.5   | 739 | 21 AAA37071 Human PRO1283 (UNQ |
| 7          | 688.8       | 99.5   | 739 | 24 ABL95663 Human anglogenesis |
| 8          | 688.8       | 99.5   | 739 | 24 ABL88174 Human PRO1283 cDNA |
| 9          | 676         | 97.7   | 676 | 22 AAF80043 Nucleotide sequenc |

|    |       |      |       |    |          |                    |
|----|-------|------|-------|----|----------|--------------------|
| 10 | 648.8 | 93.8 | 676   | 22 | AAF80039 | Nucleotide sequenc |
| 11 | 589.8 | 85.2 | 725   | 22 | AAF80040 | Nucleotide sequenc |
| 12 | 573.8 | 82.9 | 741   | 22 | AAF80041 | Nucleotide sequenc |
| 13 | 569.2 | 82.3 | 603   | 23 | AA576054 | DNA encoding novel |
| 14 | 560   | 80.9 | 782   | 22 | AAF80044 | Nucleotide sequenc |
| 15 | 543.8 | 78.6 | 781   | 22 | AAK51815 | Human polynucleoti |
| 16 | 514.4 | 74.3 | 522   | 20 | AAK19505 | Human lipocalin ho |
| 17 | 514.4 | 74.3 | 523   | 24 | AD35179  | DNA encoding novel |
| 18 | 472.2 | 68.2 | 666   | 23 | AA576055 | Nucleotide sequenc |
| 19 | 472.8 | 61.7 | 542   | 22 | AAF80045 | Degenerate lipocal |
| 20 | 372.2 | 53.8 | 510   | 20 | AAK19506 | Gene No. 32 encodi |
| 21 | 368.6 | 53.2 | 1002  | 20 | AAV08842 | Gene No. 32 encodi |
| 22 | 368.2 | 53.2 | 981   | 20 | AAV08843 | Human secreted pro |
| 23 | 337   | 47.9 | 357   | 21 | AAK03580 | Nucleotide sequenc |
| 24 | 331.2 | 47.9 | 607   | 22 | AAF80042 | Human BS124 specif |
| 25 | 329.4 | 47.6 | 245   | 20 | AAK07454 | Human BS124 specif |
| 26 | 245   | 35.4 | 245   | 20 | AAK07454 | Human BS124 specif |
| 27 | 236   | 34.1 | 236   | 20 | AAK07453 | cDNA corresponding |
| 28 | 166.6 | 24.1 | 770   | 22 | AAH74633 | DNA encoding novel |
| 29 | 153.8 | 22.2 | 2598  | 23 | AA593598 | cDNA encoding Can  |
| 30 | 145.2 | 21.0 | 525   | 15 | AAQ69950 | Human reproductive |
| 31 | 136.6 | 19.7 | 3952  | 22 | AAK03258 | Human reproductive |
| 32 | 136.6 | 19.7 | 3955  | 22 | AAK03257 | Nucleotide sequenc |
| 33 | 136.6 | 19.7 | 13591 | 22 | AAF80047 | Nucleotide sequenc |
| 34 | 135   | 19.5 | 10664 | 22 | AAF80046 | cDNA encoding VNSP |
| 35 | 132.4 | 19.1 | 774   | 17 | AAT35147 | cDNA encoding VNSP |
| 36 | 107.6 | 15.5 | 702   | 17 | AAT35146 | DNA encoding novel |
| 37 | 62.2  | 9.0  | 3348  | 23 | AA570271 | DNA encoding novel |
| 38 | 62.2  | 9.0  | 3348  | 23 | AA573851 | DNA encoding novel |
| 39 | 62.2  | 9.0  | 3348  | 23 | AA573011 | DNA encoding novel |
| 40 | 62.2  | 9.0  | 3348  | 23 | AA578956 | DNA encoding novel |
| 41 | 62.2  | 9.0  | 3348  | 23 | AA581386 | DNA encoding novel |
| 42 | 62.2  | 9.0  | 3348  | 23 | AA581677 | DNA encoding novel |
| 43 | 62.2  | 9.0  | 3348  | 23 | AA587373 | DNA encoding novel |
| 44 | 62.2  | 9.0  | 3349  | 23 | AA577495 | DNA encoding novel |
| 45 | 62.2  | 9.0  | 3349  | 23 | AA579120 | DNA encoding novel |

# ALIGNMENTS

|          |             |                                                                |                               |
|----------|-------------|----------------------------------------------------------------|-------------------------------|
| RESULT 1 | ID          | AXX07456                                                       | standard; cDNA; 692 BP.       |
| AXX07456 | AXX07456    | standard; cDNA; 692 BP.                                        |                               |
| XX       | AXX07456;   |                                                                |                               |
| XX       | 08-JUN-1999 | (first entry)                                                  |                               |
| DT       | DT          | 08-JUN-1999                                                    | (first entry)                 |
| XX       | Human BS124 | specific EST clone 17302941H.                                  |                               |
| DE       | DE          | Human BS124                                                    | specific EST clone 17302941H. |
| XX       | BS124;      | breast; cancer; detection; diagnosis; prevention; treatment;   |                               |
| KW       | KW          | EST; ss.                                                       |                               |
| XX       | XX          | Homo sapiens.                                                  |                               |
| OS       | OS          | Homo sapiens.                                                  |                               |
| XX       | XX          | WO9859049-A1.                                                  |                               |
| PN       | PN          | 30-DEC-1998.                                                   |                               |
| PD       | PD          | 30-DEC-1998.                                                   |                               |
| XX       | XX          | 19-JUN-1998;                                                   | 98WO-US12862.                 |
| PF       | PF          | 19-JUN-1998;                                                   | 98WO-US12862.                 |
| XX       | XX          | 20-JUN-1997;                                                   | 97US-0879354.                 |
| PR       | PR          | 20-JUN-1997;                                                   | 97US-0879354.                 |
| XX       | XX          | (ABBO )                                                        | ABBOTT LAB.                   |
| PA       | PA          | Billing-medell PA, Cohen M, Colpitts Tr, Friedman PN;          |                               |
| PI       | PI          | Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;     |                               |
| PI       | PI          | Russell JC, Scheffel CP, Stroupe SD, Yu H;                     |                               |
| XX       | XX          | WPI; 1999-105623/09.                                           |                               |
| DR       | DR          | New isolated BS124 polynucleotides and polypeptides - used for |                               |
| XX       | XX          |                                                                |                               |
| PT       | PT          |                                                                |                               |



Db 481 TGGTGCAGCGAAGGAGCTCTCGAGGAGGACATTTTCAAGCCCTTCGAGACGGGAAGCT 540  
Qy 541 GGGTTCGCCAAGCACTAGGAGAGCCCGGGGTCTGCACTCCAGAGCCCACTTACACACAG 600  
Db 541 GGGTTCGCCAAGCACTAGGAGAGCCCGGGGTCTGCACTCCAGAGCCCACTTACACACAG 600  
Qy 601 ACACAGAGCCCGGAGCAGCAGCTGACCTACCTCCAGAGCAGCTTCCCTCTCCACCC 660  
Db 601 ACACAGAGCCCGGAGCAGCAGCTGACCTACCTCCAGAGCAGCTTCCCTCTCCACCC 660  
Qy 661 ACCTGACTCCAAATAAGTCTTCTCCGCCA 592  
Db 661 ACCTGACTCCAAATAAGTCTTCTCCGCCA 592

RESULT 3

AAZ91770  
ID AAZ91770 standard; DNA; 690 BP.  
XX  
AC AAZ91770;  
XX  
DT 01-JUN-2000 (first entry)  
XX  
DE Human breast specific gene LS clone 1213903.  
XX  
KW Human: breast specific gene; breast specific marker; BSG; diagnosis;  
KW breast cancer; therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200008210-A1.  
XX  
PD 17-FEB-2000.  
XX  
PF 22-JUL-1999; 99WO-US16811.  
XX  
PR 04-AUG-1998; 98US-0095232.  
XX  
PA (DIAD-) DIADEXUS LLC.  
XX  
PI Sun Y, Recipon H, Cafferkey R;  
XX  
DR WPI; 2000-205737/18.  
XX  
PT Detecting, diagnosing, monitoring, staging, prognosticating, imaging  
PT and treating breast cancer using protein product of breast specific  
PT genes -  
XX  
PS Example 1; Page 43; 45pp; English.

CC This sequence represents a breast specific gene (BSG) clone. The BSG  
CC sequences are also referred to as breast specific markers (BSM). The  
CC invention relates to methods for diagnosing, monitoring, staging, imaging  
CC and treating breast cancer (BC). The methods comprise measuring the  
CC levels of BSG products in cells, tissues or body fluids of a patient  
CC and comparing the measured levels of BSG, with BSG levels of a normal  
CC human control. An antibody against the BSG sequences can be labelled and  
CC used for imaging BC in a patient. The antibody can be conjugated to a  
CC cytotoxic agent, and used for treating BC in a patient.  
XX  
SQ Sequence 690 BP; 161 A; 208 C; 205 G; 116 T; 0 other;

Query Match 99.7%; Score 690; DB 21; Length 690;  
Best Local Similarity 100.0%; Pred. No. 1.4e-167;  
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACGCCAGTGCCTCGGAGTGGGAGCAGAGCTTGGAGTGCAGACCTCTTCC 60  
Db 1 GACGCCAGTGCCTCGGAGTGGGAGCAGAGCTTGGAGTGCAGACCTCTTCC 60  
Qy 61 TGGGTGCAGCTCGGCTCGGCTGCTCTTCAAGCCCTCGAGAGGAGGATATCA 120

Db 61 TGGGTGCAGCTCGGCTCGGCTGCTCTTCAAGCCCTCGAGAGGAGGATATCA 120  
Qy 121 CAGGGACTTGTAGTGAAGCCATGTGGTTCGATGAAGAGCTTCCGGAGCAGGAGGC 180  
Db 121 CAGGGACTTGTAGTGAAGCCATGTGGTTCGATGAAGAGCTTCCGGAGCAGGAGGC 180  
Qy 181 CCAGGAAGTGTCCCAAGTGAAGGTGACAGCCCTGGGGGTFGGGAAGTGGAAAGCCACCT 240  
Db 181 CCAGGAAGTGTCCCAAGTGAAGGTGACAGCCCTGGGGGTFGGGAAGTGGAAAGCCACCT 240  
Qy 241 TCACCTTCATGAGGAGGATCGGTGCTATCCAGAGAAATCCTGATGCGGAAGAGGAGG 300  
Db 241 TCACCTTCATGAGGAGGATCGGTGCTATCCAGAGAAATCCTGATGCGGAAGAGGAGG 300  
Qy 301 AGCTGCGCAATACAGCGCTATGGGGGAGGAGCTCATGTACTTCGAGAGCTGCCCA 360  
Db 301 AGCTGCGCAATACAGCGCTATGGGGGAGGAGCTCATGTACTTCGAGAGCTGCCCA 360  
Qy 361 GGAGGACCTACATCTTTTACTGCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
Db 361 GGAGGACCTACATCTTTTACTGCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
Qy 421 GAAAGCTTGTGGTAGGAATTCGATACCAACCGGGAGGCCCTGGAGAAATTAAGAAT 480  
Db 421 GAAAGCTTGTGGTAGGAATTCGATACCAACCGGGAGGCCCTGGAGAAATTAAGAAT 480  
Qy 481 TGGTGCAGCGCAGAGGAGCTCTCGAGAGGAGACATTTTACGCCCTTCGAGAGGAGCT 540  
Db 481 TGGTGCAGCGCAGAGGAGCTCTCGAGAGGAGACATTTTACGCCCTTCGAGAGGAGCT 540  
Qy 541 GGTTCGCCAAGCACTAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600  
Db 541 GGTTCGCCAAGCACTAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600  
Qy 601 ACACAGAGCCCGGAGCAGCAGCTGACCTACCTCCAGAGCAGCTTCCCTCTCCACCC 660  
Db 601 ACACAGAGCCCGGAGCAGCAGCTGACCTACCTCCAGAGCAGCTTCCCTCTCCACCC 660  
Qy 661 ACCTGACTCCAAATAAGTCTTCTCCGCC 690  
Db 661 ACCTGACTCCAAATAAGTCTTCTCCGCC 690

RESULT 4

AAF54313  
ID AAF54313 standard; DNA; 738 BP.  
XX  
AC AAF54313;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE DNA encoding protein of the invention #50.  
XX  
KW Secreted; transmembrane; gene therapy; ss.  
XX  
OS Unidentified.  
XX  
PN WO200078961-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 18-FEB-2000; 2000WO-US04342.  
XX  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28551.  
PR 16-DEC-1999; 99WO-US30095.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.

XX (GETH) GENENTECH INC.  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Pan J, Peoni NF, Roy MA, Smith V, Stewart TA, Tumas D;  
PI Watanabe CK, Williams PM, Wood WL;  
XX WPI; 2001-071395/08.  
XX  
XX Secreted and transmembrane proteins and nucleic acids designated PRO.  
PT useful as hybridization probes, in chromosome and gene mapping and gene  
PA therapy -  
XX  
XX Claim 2; Fig 99; 787pp; English.  
XX  
XX The present invention relates to secreted and transmembrane proteins.  
CC These proteins and the DNA encoding them may be used as hybridization  
CC probes, in chromosome and gene mapping and in the generation of  
CC anti-sense RNA and DNA. They may also be used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents.  
CC The nucleic acids may also be used in gene therapy.  
XX  
XX Sequence 738 BP; 209 A; 207 C; 205 G; 117 T; 0 other;  
SQ  
Query Match 99.5%; Score 688.8; DB 22; Length 738;  
Best Local Similarity 99.7%; Pred. No. 2.8e-167;  
Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAGCGCAGTGTGCTCCGAGTGGCGGACACAGAGCTCTGGAGATGAAGACCTGTTC 60  
DB 1 GAGCGCAGTGTGCTCCGAGTGGCGGACACAGAGCTCTGGAGATGAAGACCTGTTC 60  
QY 61 TGGGTGTACGCTGGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 61 TGGGTGTACGCTGGCTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
QY 121 CAGGAGCTGTGCTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
DB 121 CAGGAGCTGTGCTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
QY 181 CCAGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 CCAGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 TCACCTTCATGAGGAGGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 241 TCACCTTCATGAGGAGGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
QY 301 AGCTGTCGAATACAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 301 AGCTGTCGAATACAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 361 GGAGGACACTTACATCTTTTCTGCAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
DB 361 GGAGGACACTTACATCTTTTCTGCAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
QY 421 GAAAGCTGTGGTAGGAATTTCTGATACCAACCGGAGGCGCTTGAAGAATTTAAGAAT 480  
DB 421 GAAAGCTGTGGTAGGAATTTCTGATACCAACCGGAGGCGCTTGAAGAATTTAAGAAT 480  
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DB 481 TGGTGCAGCGCAAGGAGCTGTGAGGAGGAGCAATTTTACGCGCTTGCAGAGCGGAAGCT 540  
QY 541 GCGTTCGCACTAGGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
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QY 601 ACACAGAGCGGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
DB 601 ACACAGAGCGGAGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 661 ACCTGACTCCAAATAAAGTCTTCTCCOCCCA 692  
DB 661 ACCTGACTCCAAATAAAGTCTTCTCCOCCCA 692  
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ID AAC58615 standard; cDNA; 739 BP.  
XX AAC58615;  
AC AAC58615;  
XX 29-JAN-2001 (first entry)  
XX Human PRO1283 protein UNQ653 encoding cDNA SEQ ID NO:169.  
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW hemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.  
XX Homo sapiens.  
XX WO200053758-A2.  
XX 14-SEP-2000.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28584.  
PR 16-DEC-1999; 99WO-US28565.  
PR 20-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.





|    |              |               |    |                                                                         |               |    |                                                                         |   |
|----|--------------|---------------|----|-------------------------------------------------------------------------|---------------|----|-------------------------------------------------------------------------|---|
| PR | 17-SEP-1998; | 98US-0100684. | PR | 03-NOV-1998;                                                            | 98US-0106919. | CC | AAA37022 to AAA37144 encode the new isolated human transmembrane,       | 0 |
| PR | 17-SEP-1998; | 98US-0100710. | PR | 03-NOV-1998;                                                            | 98US-0106932. | CC | receptor or secreted PRO polypeptides given in AA99340 to AA99462. The  | 0 |
| PR | 17-SEP-1998; | 98US-0100711. | PR | 03-NOV-1998;                                                            | 98US-0106934. | CC | transmembrane and receptor PRO proteins can be used for screening of    | 0 |
| PR | 17-SEP-1998; | 98US-0100919. | PR | 10-NOV-1998;                                                            | 98US-0107783. | CC | potential peptide or small molecule inhibitors of the relevant          | 0 |
| PR | 17-SEP-1998; | 98US-0100930. | PR | 17-NOV-1998;                                                            | 98US-0108775. | CC | receptor/ligand interactions. The polypeptides and nucleotide sequences | 0 |
| PR | 18-SEP-1998; | 98US-0100848. | PR | 17-NOV-1998;                                                            | 98US-0108779. | CC | encoding then have various industrial applications, including uses as   | 0 |
| PR | 18-SEP-1998; | 98US-0100849. | PR | 17-NOV-1998;                                                            | 98US-0108787. | CC | pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent    | 0 |
| PR | 18-SEP-1998; | 98US-0101014. | PR | 17-NOV-1998;                                                            | 98US-0108788. | CC | PCR primers and hybridisation probes used in the isolation of the PRO   | 0 |
| PR | 18-SEP-1998; | 98US-0101068. | PR | 17-NOV-1998;                                                            | 98US-0108801. | CC | polypeptides from the present invention.                                | 0 |
| PR | 18-SEP-1998; | 98US-0101071. | PR | 17-NOV-1998;                                                            | 98US-0108802. | CC |                                                                         | 0 |
| PR | 22-SEP-1998; | 98US-0101279. | PR | 17-NOV-1998;                                                            | 98US-0108806. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101471. | PR | 17-NOV-1998;                                                            | 98US-0108807. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101472. | PR | 17-NOV-1998;                                                            | 98US-0108867. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101474. | PR | 17-NOV-1998;                                                            | 98US-0108925. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101475. | PR | 18-NOV-1998;                                                            | 98US-0108848. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101476. | PR | 18-NOV-1998;                                                            | 98US-0108849. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101477. | PR | 18-NOV-1998;                                                            | 98US-0108850. | CC |                                                                         | 0 |
| PR | 23-SEP-1998; | 98US-0101478. | PR | 18-NOV-1998;                                                            | 98US-0108851. | CC |                                                                         | 0 |
| PR | 24-SEP-1998; | 98US-0101739. | PR | 18-NOV-1998;                                                            | 98US-0108852. | CC |                                                                         | 0 |
| PR | 24-SEP-1998; | 98US-0101741. | PR | 18-NOV-1998;                                                            | 98US-0108858. | CC |                                                                         | 0 |
| PR | 24-SEP-1998; | 98US-0101743. | PR | 18-NOV-1998;                                                            | 98US-0108859. | CC |                                                                         | 0 |
| PR | 24-SEP-1998; | 98US-0101915. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 24-SEP-1998; | 98US-0101916. | PA |                                                                         |               | PA | (GETH ) GENENTECH INC.                                                  | 0 |
| PR | 29-SEP-1998; | 98US-0102207. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 29-SEP-1998; | 98US-0102240. | PI | Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;           |               | PI |                                                                         | 0 |
| PR | 29-SEP-1998; | 98US-0102307. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 29-SEP-1998; | 98US-0102330. | DR | WPI: 2000-237871/20.                                                    |               | DR |                                                                         | 0 |
| PR | 29-SEP-1998; | 98US-0102331. | DR | P-PSDB; AA99389.                                                        |               | DR |                                                                         | 0 |
| PR | 30-SEP-1998; | 98US-0102484. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 30-SEP-1998; | 98US-0102487. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 30-SEP-1998; | 98US-0102570. | PI | New mammalian DNA sequences encoding transmembrane, receptor or         |               | PI |                                                                         | 0 |
| PR | 30-SEP-1998; | 98US-0102571. | PI | secreted PRO polypeptides, useful for screening of potential peptide or |               | PI |                                                                         | 0 |
| PR | 01-OCT-1998; | 98US-0102584. | XX | small molecule inhibitors of the relevant receptor/ligand interactions  |               | XX |                                                                         | 0 |
| PR | 01-OCT-1998; | 98US-0102687. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 02-OCT-1998; | 98US-0102688. | XX | Claim 2; Fig 99; 773pp; English.                                        |               | XX |                                                                         | 0 |
| PR | 06-OCT-1998; | 98US-0102689. | XX |                                                                         |               | XX |                                                                         | 0 |
| PR | 08-OCT-1998; | 98US-0103258. | CC |                                                                         |               | CC |                                                                         | 0 |
| PR | 08-OCT-1998; | 98US-0103449. | CC | AAA37022 to AAA37144 encode the new isolated human transmembrane,       |               | CC |                                                                         | 0 |
| PR | 07-OCT-1998; | 98US-0103314. | CC | receptor or secreted PRO polypeptides given in AA99340 to AA99462. The  |               | CC |                                                                         | 0 |
| PR | 07-OCT-1998; | 98US-0103315. | CC | transmembrane and receptor PRO proteins can be used for screening of    |               | CC |                                                                         | 0 |
| PR | 07-OCT-1998; | 98US-0103328. | CC | potential peptide or small molecule inhibitors of the relevant          |               | CC |                                                                         | 0 |
| PR | 07-OCT-1998; | 98US-0103395. | CC | receptor/ligand interactions. The polypeptides and nucleotide sequences |               | CC |                                                                         | 0 |
| PR | 07-OCT-1998; | 98US-0103396. | CC | encoding then have various industrial applications, including uses as   |               | CC |                                                                         | 0 |
| PR | 07-OCT-1998; | 98US-0103401. | CC | pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent    |               | CC |                                                                         | 0 |
| PR | 08-OCT-1998; | 98US-0103633. | CC | PCR primers and hybridisation probes                                    |               |    |                                                                         |   |

Db 301 AGCTGGCAAAATACAGCCCTATGCGGGGAGGAGACTCATGTACTCTCAGGAGCTGCCCA 360  
QY 361 GGAGGACCACTACATCTTTTACTCTCAAGACACAGACATGGGGGCTGTCTCCACATGG 420  
Db 361 GGAGGACCACTACATCTTTTACTCTCAAGACACAGACATGGGGGCTGTCTCCACATGG 420  
QY 421 GAAAGCTGTGGGTAGAGATTTCTGATACCAACCGGAGGCGCTGGAAGATTTAGAAAT 480  
Db 421 GAAAGCTGTGGGTAGAGATTTCTGATACCAACCGGAGGCGCTGGAAGATTTAGAAAT 480  
QY 481 TGGTGCAGCAGGAGGACTCTCGGAGGAGGACATTTTCAGCGCCCTCGAGAGGAAGCT 540  
Db 481 TGGTGCAGCAGGAGGACTCTCGGAGGAGGACATTTTCAGCGCCCTCGAGAGGAAGCT 540  
QY 541 GGTTCGCGAACAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
Db 541 GGTTCGCGAACAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 601 ACAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
Db 601 ACAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
QY 661 ACTGACTTCCAAATAAAGTCTTCTCCGCCCA 692  
Db 661 ACTGACTTCCAAATAAAGTCTTCTCCGCCCA 692

RESULT 7  
ABL95663  
ID ABL95663 standard; cDNA; 739 BP.  
XX  
AC ABL95663;  
XX  
DT 19-JUL-2002 (first entry)  
DE Human angiotensin related cDNA PRO1283 SEQ ID NO: 205.  
XX  
KW Human; angiotensin; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiast; cytotatic; antiangiogenic; hypotensive; vulnerary;  
KW antiarteriosclerotic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208284-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 09-JUL-2001; 2001WO-0821735.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000US-0520710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-0823522.  
PR 24-AUG-2000; 2000WO-0823528.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 10-NOV-2000; 2000WO-0830952.  
PR 01-DEC-2000; 2000WO-0830873.  
PR 20-DEC-2000; 2000US-074259.  
PR 20-DEC-2000; 2000WO-0834956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-0806520.  
PR 01-MAR-2001; 2001WO-0806666.

PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0806899.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0826366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-086028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001US-087092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.  
XX (GETH ) GENENTECH INC.  
PA (BAKE) BAKER K P.  
PA (FERE) FERRARA N.  
PA (GERR) GERBER H.  
PA (GERR) GERRITSEN M E.  
PA (GODD) GODDARD A.  
PA (GODO) GODOWSKI P J.  
PA (GURN) GURNEY A L.  
PA (HILL) HILLAN K J.  
PA (MARS) MARSTERS S A.  
PA (PANJ) PAN J.  
PA (PAOM) PAONI N F.  
PA (STEP) STEPHAN J F.  
PA (WATA) WATANABE C K.  
PA (WILL) WILLIAMS P M.  
PA (WOOD) WOOD W I.  
XX  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski BJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
XX WPI: 2002-171999/22.  
DR P-PSDB; ABB95525.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
XX Claim 1; Fig 205; 567pp; English.  
XX  
XX The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.  
XX  
XX Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;  
SQ

Query Match 99.5%; Score 688.8; DB 24; Length 739;  
Best Local Similarity 99.7%; Pred. No. 2.9e-167;  
Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GACGCCAGTGACCTGCGGAGGTCGCGACACAGAGCTGTGGAGATCAAGACCTGTGTC 60  
Db 1 GACGCCAGTGACCTGCGGAGGTCGCGACACAGAGCTGTGGAGATCAAGACCTGTGTC 60  
QY 61 TGGGTGTGTCAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 120  
Db 61 TGGGTGTGTCAGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 120  
QY 121 CAGGAGCTGTGACGTGAAGGCCATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180  
Db 121 CAGGAGCTGTGACGTGAAGGCCATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180  
QY 181 CCAGGAGGAGTGTCTCCAGTGAAGGTGACAGCCCTGCGGCGGTGGAGAGTGTGGAAGCCACGT 240



181 CCAGGAGGTGTCCCACTGAAGTGCAGCCCTGGCGGTGGAGTGTGGAGCCACGT 240  
181 CCAGGAGGTGTCCCACTGAAGTGCAGCCCTGGCGGTGGAGTGTGGAGCCACGT 240  
241 TCACCTTCATGAGGAGGATCGGTGCATCCAGAGAAATCTGTATGCGAGAGCGAGG 300  
241 TCACCTTCATGAGGAGGATCGGTGCATCCAGAGAAATCTGTATGCGAGAGCGAGG 300  
301 AGCTGGCAATACAGCCCTATGGGGCAGGAGCTCATGTACTGCAGAGCTGCCCA 360  
301 AGCTGGCAATACAGCCCTATGGGGCAGGAGCTCATGTACTGCAGAGCTGCCCA 360  
361 GGAGGACACATCACTTTTACTGCAAGACCCAGCAGCATGGGGCTGCTCCACATGG 420  
361 GGAGGACACATCACTTTTACTGCAAGACCCAGCAGCATGGGGCTGCTCCACATGG 420  
421 GAAAGTTGGGTAGGAATTCGATFACCAACCGGAGGCGCTTGAGAGATTTAGAAAT 480  
421 GAAAGTTGGGTAGGAATTCGATFACCAACCGGAGGCGCTTGAGAGATTTAGAAAT 480  
481 TGGTGACGCAAGGAGCTCTCGAGGAGGAGACATTTTCACGCGCTTGAGAGGAAAGCT 540  
481 TGGTGACGCAAGGAGCTCTCGAGGAGGAGACATTTTCACGCGCTTGAGAGGAAAGCT 540  
541 GCGTTCGCAACACTAGGAGCGCCCGGGGTCTGCACCTCCAGAGCGCCACCTACCAACAG 600  
541 GCGTTCGCAACACTAGGAGCGCCCGGGGTCTGCACCTCCAGAGCGCCACCTACCAACAG 600  
601 ACACAGAGCCGAGCACTGACCTACCTCCAGCATGACCTTCCTGCTCCACCC 660  
601 ACACAGAGCCGAGCACTGACCTACCTCCAGCATGACCTTCCTGCTCCACCC 660  
661 ACCTGACTCCAAATTAAGTCTTCGCCCA 692  
661 ACCTGACTCCAAATTAAGTCTTCGCCCA 692

RESULT 9  
AAAF0043  
ID AAF80043 standard; cDNA; 676 BP.  
AC AAF80043;  
XX  
DT 11-JUN-2001 (first entry)  
XX  
DE Nucleotide sequence of odorant binding polypeptide OBPIB-alpha.  
XX  
KW Odorant binding polypeptide; OBPI; hydrophobic ligand; odorant; allergy;  
KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;  
KW anticancer; foetus detoxification; pregnancy marker; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 43..555  
FT /tag- a  
FT /product= "odorant binding polypeptide OBPIB-alpha"  
XX  
XX WO200112806-A2.  
XX  
XX 22-FEB-2001.  
XX  
XX 11-AUG-2000; 2000WO-FR02319.  
XX  
XX 12-AUG-1999; 99FR-0010439.  
XX (UYAU-) UNIV ADVERGNE.  
XX PA (PIPI/) PIPIOT G.  
XX  
XX PIPIOT G, Lacazette E, Gachon F;  
XX  
XX WFI; 2001-202864/20.

P-PSDB; AAB67742.  
New human odorant-binding proteins, useful for solubilising lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes  
Disclosure: Page 113-114; 132pp; French.  
The present sequence encodes a human odorant binding polypeptide (OBP), designated OBPIB-alpha. OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc.. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity; or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foeto-placental pathology (rupture of the amniotic membrane); and as anti-allergic agents.  
Sequence 676 BP; 160 A; 200 C; 204 G; 112 T; 0 other;  
Query Match 97.7%; Score 676; DB 22; Length 676;  
Best Local Similarity 100.0%; Pred. No. 5.4e-164;  
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
3 CGCCAGTGTACCTGCGGAGTGGCAGCAGACAGCTCTGGAGATGAAGACCTGTCTCTG 62  
1 CGCCAGTGTACCTGCGGAGTGGCAGCAGACAGCTCTGGAGATGAAGACCTGTCTCTG 60  
63 GGTGTGACGTGTGGCGGCTGCTGCTCTTCCCTGCTGAGGAGGAGGATATCACA 122  
61 GGTGTGACGTGTGGCGGCTGCTGCTCTTCCCTGCTGAGGAGGAGGATATCACA 120  
123 GGGACCTGTGTACGTGAGGCGCATGTGTGTGATGAGGACTTTCGGGAGCAGCGAGCC 182  
121 GGGACCTGTGTACGTGAGGCGCATGTGTGTGATGAGGACTTTCGGGAGCAGCGAGCC 180  
183 AGGAAGTGTGCCCAAGTGAAGTGCAGCCCTGCGGCGGTGGGAGTGTGGAACCACTTC 242  
181 AGGAAGTGTGCCCAAGTGAAGTGCAGCCCTGCGGCGGTGGGAGTGTGGAACCACTTC 240  
243 ACCTTCATGAGGAGGATCGGTGTGATCCAGAGAAATCTGATCGGAGAGCGAGGAG 302  
241 ACCTTCATGAGGAGGATCGGTGTGATCCAGAGAAATCTGATCGGAGAGCGAGGAG 300  
303 CTGCGCAATATACAGCGCTATGGGGCAGGAGCTCATGTACTGCAGAGAGTGCACAGG 362  
301 CTGCGCAATATACAGCGCTATGGGGCAGGAGCTCATGTACTGCAGAGAGTGCACAGG 360  
363 AGGGACACTACATCTTTTACTGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 422  
361 AGGGACACTACATCTTTTACTGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
423 AGCTTGTGGGTAGGATCTGTATGATCAACCGGGGCGCTTGAGAGATTTAGAAATTC 482  
421 AGCTTGTGGGTAGGATCTGTATGATCAACCGGGGCGCTTGAGAGATTTAGAAATTC 480  
483 GTCCAGCCCAAGGAGCTCTCGAGGAGGACATTTTCAGCCCTCTCAGAGGAGAGCTGC 542  
481 GTCCAGCCCAAGGAGCTCTCGAGGAGGACATTTTCAGCCCTCTCAGAGGAGAGCTGC 540  
543 GTTCCCGAACACTAGGAGAGCCCGGGGTGTCACCTCCAGAGCCACCTTACCCAGAG 602  
541 GTTCCCGAACACTAGGAGAGCCCGGGGTGTCACCTCCAGAGCCACCTTACCCAGAG 600

QY 603 ACAGAGCCGGGACCACTGGACCTACCTCCAGCAGCATGACCTCCCTGCTCCACCCAC 662  
 DB 601 ACAGAGCCGGGACCACTGGACCTACCTCCAGCAGCATGACCTCCCTGCTCCACCCAC 660  
 QY 663 CTGACTCCAAATAAG 678  
 DB 661 CTGACTCCAAATAAG 676

## RESULT 10

AAF80039 standard; cDNA; 676 BP.

XX AAF80039;

DT 11-JUN-2001 (first entry)

DE Nucleotide sequence of odorant binding polypeptide OBPIIa-alpha.

XX Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy;  
 KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;  
 KW anticancer; foetus detoxification; pregnancy marker; ss.

XX Homo sapiens.

PH Key Location/Qualifiers

FT 43..555

FT /tag= a

FT /product= "odorant binding polypeptide OBPIIa-alpha"

FN WO200112806-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-FR02319.

PR 12-AUG-1999; 99FR-0010439.

PA (UYAU)/ UNIV AUVERGNE.

PA (PITI)/ PITIOT G.

PI Pitiot G, Lacazette E, Gachon E;

PI WPI; 2001-202864/20.

DR P-PSDB; AAB67738.

XX New human odorant-binding proteins, useful for solubilising lipophilic  
 FT compounds in the transportation of anticancer agents or for slow  
 FT release of perfumes

XX Claim 6; Page 106-107; 132pp; French.

XX The present sequence encodes a human odorant binding polypeptide (OBP),  
 CC designated OBPIIa-alpha. OBPs provide long-term retention (gradual  
 CC release) of lipophilic compounds, so prolong the 'hold' of perfumes,  
 CC deodorants etc.. OBP polypeptides are used as binding proteins for  
 CC hydrophobic ligands (particularly odorants); as competitive inhibitors  
 CC (agonists or antagonists) of cellular lipocalin receptors; to detect  
 CC specific antibodies for diagnosis of allergy, asthma or cancer; for  
 CC controlling volatilisation of an odorant, specifically in perfumes,  
 CC cosmetics or disinfectant compositions; to screen compounds, especially  
 CC odorants or flavours, e.g. human pheromones, for binding to OBP, also in  
 CC analysis of complex perfume mixtures; to solubilise lipophilic compounds;  
 CC for treating hyperlipidemia or obesity, or to supplement non-maternal  
 CC milk when combined with nutritional fatty acids, as food additives; as a  
 CC transporter of pharmaceuticals, especially anticancer agents (providing  
 CC delayed release) but also for delivery across the placental barrier  
 CC (e.g. for detoxification of the foetus); as a marker of pregnancy or  
 CC foeto-placental pathology (rupture of the amniotic membrane); and as  
 CC anti-allergic agents.

XX Sequence 676 BP; 158 A; 199 C; 204 G; 115 T; 0 other;

Query Match 93.8%; Score 648.8; DB 22; Length 676;  
 Best Local Similarity 97.5%; Pred. No. 5.2e-157;  
 Matches 659; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CGCCAGTGACCTGCGGAGGTGCGGACACACAGAGCTCTGGAGATGAAGACCTGTCTCTG 62

DB 1 CGCCAGTGACCTGCGGAGGTGCGGACACACAGAGCTCTGGAGATGAAGACCTGTCTCTG 60

QY 63 GGTGTACGCTCGGCTGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 122

DB 61 GGTGTACGCTCGGCTGGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120

QY 123 GGGACCTGTGTACGTGAGGCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 182

DB 121 GGGACCTGTGTACGTGAGGCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180

QY 183 AGAAGGTGTCCCGAGTGAAGGTGACAGCCCTGTGGGCGGTGGGAGTGTGGAGCCACGTTTC 242

DB 181 AGAAGGTGTCCCGAGTGAAGGTGACAGCCCTGTGGGCGGTGGGAGTGTGGAGCCACGTTTC 240

QY 243 ACCTTCATGAGGAGGATCGGTGCATCCAGAGCAAAATCTGTATCGGAGAGAGGAGAG 302

DB 241 ACCTTCATGAGGAGGATCGGTGCATCCAGAGCAAAATCTGTATCGGAGAGAGGAGAG 300

QY 303 CTGCGCAATACACAGCGCTATGGGGGAGGAGTCAATGCTACCTCAGAGAGTGCACGAGG 362

DB 301 CTGCGCAATACACAGCGCTATGGGGGAGGAGTCAATGCTACCTCAGAGAGTGCACGAGG 360

QY 363 AGGACCACTACATCTCTTACTGCAAGACACGACCATGGGGGCTGCTCCACATGGGA 422

DB 361 AGGACCACTACATCTCTTACTGCAAGACACGACCATGGGGGCTGCTCCACATGGGA 420

QY 423 AAGCTTGTGGTAGGAATCTGTATACCAACCGGAGGCGCTGTGGAAGATTTAGAAATTC 482

DB 421 AAGCTTGTGGTAGGAATCTGTATACCAACCGGAGGCGCTGTGGAAGATTTAGAAATTC 480

QY 483 GTGACGCCAAGGGACTCTCGGAGGAGGACATTTTCAGGCCCTCGACAGCGGAAGTGC 542

DB 481 GTGACGCCAAGGGACTCTCGGAGGAGGACATTTTCAGGCCCTCGACAGCGGAAGTGC 540

QY 543 GTTCCGGAACACTAGGACAGCCCGGCGGTGTGACCTCCAGAGCCACCTTCCCTGCTCCACCCAC 602

DB 541 GTTCCGGAACACTAGGACAGCCCGGCGGTGTGACCTCCAGAGCCACCTTCCCTGCTCCACCCAC 600

QY 603 ACAGAGCCGGGACCACTGGACCTACCTCCAGCAGCATGACCTCCCTGCTCCACCCAC 662

DB 601 ACAGAGCCGGGACCACTGGACCTACCTCCAGCAGCATGACCTCCCTGCTCCACCCAC 660

QY 663 CTGACTCCAAATAAG 678

DB 661 CTGACTCCAAATAAG 676

## RESULT 11

AAF80040 standard; cDNA; 725 BP.

XX AAF80040;

DT 11-JUN-2001 (first entry)

DE Nucleotide sequence of odorant binding polypeptide OBPIIa-beta.

XX Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy;  
 KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;  
 KW anticancer; foetus detoxification; pregnancy marker; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT 43..483

FT /\*tag= a

FT /product= "odorant binding polypeptide OBPIIa-beta"



release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc.. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavourors, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds for treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foeto-placental pathology (rupture of the amniotic membrane); and as anti-allergic agents.

Sequence 741 BP; 165 A; 229 C; 220 G; 127 T; 0 other;

Query Match 82.9%; Score 573.8; DB 22; Length 741;  
Best Local Similarity 88.9%; Pred. No. 1e-137;  
Matches 659; Conservative 0; Mismatches 17; Indels 65; Gaps

|    |     |                                                                 |     |
|----|-----|-----------------------------------------------------------------|-----|
| QY | 3   | CGCCACGTGACCTCGCGAGTGTGGCGACACAGAGCTCTGGAGATGAGACACCTGTCTCTG    | CG  |
| DB | 1   | CGCCACGTGACCTCGCGAGTGTGGCGACACAGAGCTCTGGAGATGAGACACCTGTCTCTG    | CG  |
| DB | 60  | CGCCACGTGACCTCGCGAGTGTGGCGACACAGAGCTCTGGAGATGAGACACCTGTCTCTG    | CG  |
| QY | 63  | GGTGTACAGCTCGGCGTCTGGCGCGTGGCTGTCTTCACCTCGAGAGAGAGATATACCA      | 122 |
| DB | 61  | GGTGTACAGCTCGGCGTCTGGCGCGTGGCTGTCTTCACCTCGAGAGAGAGATATACCA      | 120 |
| QY | 123 | GGGACCTGTGTACGTGAAGGCCATGGTGGPCGATAAGGACTTCCGSGAGGACAGGAGGCC    | 182 |
| DB | 121 | GGGACCTGTGTACGTGAAGGCCATGGTGGPCGATAAGGACTTCCGSGAGGACAGGAGGCC    | 180 |
| QY | 183 | AGGAAGTGTCTCCCAAGTGAAGGTACAGACCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTTC | 242 |
| DB | 181 | AGGAAGTGTCTCCCAAGTGAAGGTACAGACCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTTC | 240 |
| QY | 243 | ACCTTCATGAGGAGGAGTACGTGTGATCCAGAGAATAAATCTGTATCGGAAGACGAGGAG    | 302 |
| DB | 241 | ACCTTCATGAGGAGGAGTACGTGTGATCCAGAGAATAAATCTGTATCGGAAGACGAGGAG    | 300 |
| QY | 303 | CCTGGCAATATACAGCGCTATGGGGGCGAGGAAGCTCATGTACTGTCAGGAGCTGCCACG    | 362 |
| DB | 301 | CCTGGCAATATACAGCGCTATGGGGGCGAGGAAGCTCATATACCTTCAGGAGCTGCCACG    | 360 |
| QY | 363 | AGGAGCACTATCATCTTTTACTGTCAAAGACACAGACATGGGGGCGCTCTCCACATGGGA    | 422 |
| DB | 361 | AGGAGCACTATCATCTTTTACTGTCAAAGACACAGACATGGGGGCGCTCTCCACATGGGA    | 420 |
| QY | 423 | AAAGCTTGTC-----                                                 | 431 |
| DB | 421 | AAAGCTTGTCGATCTGCTCCTCTCGAGGGCGGTGCGCTGTCCCAACGTGSGCTCACTGG     | 480 |
| QY | 432 | -----GGTAGAATTCGTATACCAACCGGAGGAGCCCTGAGAGATTTAAGA              | 477 |
| DB | 481 | CCACCTCACTCGAGGTGATGATCTTAATACCAACCTCGAGGCGCTCGAGATTTAAGA       | 540 |
| QY | 478 | AATTGGTCAGCGCAGGAGACTCTTCGAGGAGGAGCATTTTCAGCGCCCTCGAGAGGGA      | 537 |
| DB | 541 | AATTGGTCAGCGCAGGAGACTCTTCGAGGAGGAGCATTTTCAGCGCCCTCGAGAGGGA      | 600 |
| QY | 538 | GCTGGGTTTCCGACACATAGGAGAGCCCGCGGGTCTGCACTTCAGAGGCCACCTTACAC     | 597 |
| DB | 601 | GCTGGGTTTCCGACACATAGGAGAGCCCGCGGGTCTGCACTTCAGAGGCCACCTTACAC     | 660 |
| QY | 598 | CAGACACAGACCGCGGACCACTGGACCTTACCTTCAGGCATGACCTTCCTTCCTCCCA      | 657 |
| DB | 661 | CAGACACAGACCGCGGACCACTGGACCTTACCTTCAGGCATGACCTTCCTTCCTCCCA      | 720 |
| QY | 658 | CCACCTTGACTCCAAATAAAG                                           | 678 |

|    |           |                                                                                                  |     |
|----|-----------|--------------------------------------------------------------------------------------------------|-----|
| Db | 721       | CCCACTGACTCCAAATAAAG                                                                             | 741 |
|    | RESULT 13 |                                                                                                  |     |
|    | AA576054  |                                                                                                  |     |
| XX | ID        | AA576054 standard; cDNA; 603 BP.                                                                 |     |
| XX | AC        | AA576054;                                                                                        |     |
| XX | DT        | 13-FEB-2002 (first entry)                                                                        |     |
| XX | DE        | DNA encoding novel human diaphorase                                                              |     |
| XX | DE        | Human; chromosome mapping; gene                                                                  |     |
| XX | KW        | food supplement; medical imaging                                                                 |     |
| XX | OS        | Homo sapiens.                                                                                    |     |
| XX | XX        | WO200175067-A2.                                                                                  |     |
| XX | PN        | 11-OCT-2001.                                                                                     |     |
| XX | PD        | 30-MAR-2001; 2001WO-US08631.                                                                     |     |
| XX | PF        | 21-MAR-2000; 2000US-0540217.                                                                     |     |
| XX | PR        | 23-AUG-2000; 2000US-0649167.                                                                     |     |
| XX | PR        | (HYSE-) HYSE INC.                                                                                |     |
| XX | PA        | Drmanac RT, Liu C, Tang YT;                                                                      |     |
| XX | PI        | WT: 2001-639362/73.                                                                              |     |
| XX | PI        | P-PSDB; ABG11867.                                                                                |     |
| XX | DR        | New isolated polynucleotide and                                                                  |     |
| XX | DR        | diagnostics; forensics, gene mapping                                                             |     |
| XX | PT        | responsible for genetic disorder.                                                                |     |
| XX | PT        | Biodiversity -                                                                                   |     |
| XX | PT        | Claim 1; SEQ ID No 11859; 103pp;                                                                 |     |
| XX | PS        | The invention relates to isolated                                                                |     |
| XX | CC        | polypeptide (II) sequences. (I)                                                                  |     |
| XX | CC        | polymerase chain reaction (PCR)                                                                  |     |
| XX | CC        | and gene mapping, and in recombina                                                               |     |
| XX | CC        | polynucleotides are also used in                                                                 |     |
| XX | CC        | for identifying expressed genes.                                                                 |     |
| XX | CC        | to restore normal activity of (I)                                                                |     |
| XX | CC        | (II). (II) is useful for generat                                                                 |     |
| XX | CC        | quantitating a polypeptide in ti                                                                 |     |
| XX | CC        | a food supplement. (II) and its                                                                  |     |
| XX | CC        | imaging of sites expressing (II)                                                                 |     |
| XX | CC        | disorders involving aberrant pro                                                                 |     |
| XX | CC        | the polypeptide and polynucleoti                                                                 |     |
| XX | CC        | diagnostics forensics, gene map                                                                  |     |
| XX | CC        | responsible for genetic disorder.                                                                |     |
| XX | CC        | and to produce other types of da                                                                 |     |
| XX | CC        | amino acid sequences. AA564197-A                                                                 |     |
| XX | CC        | diagnostic coding sequences of t                                                                 |     |
| XX | CC        | Note: The sequence data for this                                                                 |     |
| XX | CC        | specification, but was obtained                                                                  |     |
| XX | CC        | at <a href="http://www.ncbi.nlm.nih.gov/seq/submit/">http://www.ncbi.nlm.nih.gov/seq/submit/</a> |     |
| XX | CC        | Sequence 603 BP; 142 A; 178 C; 1                                                                 |     |

|    | Query Match           | 82.3%                                                         | Score 569.2;        | DB 23;        | Length 603;        |
|----|-----------------------|---------------------------------------------------------------|---------------------|---------------|--------------------|
|    | Best Local Similarity | 96.5%                                                         | Prod. No. 1.4e-136; |               |                    |
|    | Matches 600;          | Conservative                                                  | 0;                  | Mismatches 3; | Indels 19; Gaps 1; |
| QY | 45                    | ATGAAGACCTGTTCTCTGGGTGTCAAGTCTGGCGCTGGCGCTGCCCTGCTCTTCACCCCTG | 104                 |               |                    |
| Db | 1                     | ATGAAGACCTGTTCTCTGGGTGTCAAGTCTGGCGCTGGCGCTGCCCTGCTCTTCACCCCTG | 60                  |               |                    |





|||||  
541 GAAATCTGATACACCGGGGCGCTGGAGAAATTAAGAAATGTCGACGCAAGG 600  
QY 497 ACTCTGGAGAGAGACATTTTACCGCCCTGCGACGCGGAGCTCCGTCGCCGACACTA 556  
|||||  
601 ACTCTGGAGAGAGACATTTTACCGCCCTGCGACGCGGAGCTCCGTCGCCGACACTA 560  
QY 557 GGCAGCGCCCGGGTCTGACCTCCAGAGCGCCCTACACACGACGACGCGCGACC 616  
|||||  
661 GGCAGCGCCCGGGTCTGACCTCCAGAGCGCCCTACACACGACGACGCGCGACC 720  
QY 617 ACTCTGGAGAGAGACATTTTACCGCCCTGCGACGCGGAGCTCCGTCGCCGACACTA 676  
|||||  
721 ACTCTGGAGAGAGACATTTTACCGCCCTGCGACGCGGAGCTCCGTCGCCGACACTA 780  
QY 677 AG 678  
||  
781 AG 782  
||  
RESULT 15  
AAK51815  
ID AAK51815 standard; cDNA; 781 BP.  
AC AAK51815;  
XX 06-NOV-2001 (first entry)  
DT Human polynucleotide SEQ ID NO 360.  
DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
XX Homo sapiens.  
XX WO200157190-A2.  
PN 09-AUG-2001.  
EP 05-FEB-2001; 2001WO-US04098.  
XX 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0596075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX (HYSE-) HYSEQ INC.  
XX Tang Y, Liu C, Drmanac R, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao Q, Wang D, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX WPI; 2001-476283/51.  
DR P-PSDB; AAM78682.  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -  
XX Claim 1; Page 1381-1382; 622pp; English.  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapies. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80202) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.  
XX  
SQ Sequence 781 BP; 172 A; 234 C; 233 G; 142 T; 0 other;  
Query Match 78.6%; Score 543.8; DB 22; Length 781;  
Best Local Similarity 88.5%; Pred. No. 5.2e-130;  
Matches 629; Conservative 0; Mismatches 17; Indels 65; Gaps 1;  
QY 21 GGTGCGAGACAGAGCTCTGGAGATGAAGACCTCTCTGGGTGTCAGCTCGGCTG 80  
DB 71 GGTGCGAGACAGAGCTCTGGAGATGAAGACCTCTCTGGGTGTCAGCTCGGCTG 130  
QY 81 GCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 140  
DB 131 GCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 190  
QY 141 GCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 200  
DB 191 GCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250  
QY 201 AAGGTGACAGCTCTGGGCTGGGAACTTGGAAAGCCACGTTTCACTTCATGAGGAGAT 260  
DB 251 AAGGTGACAGCTCTGGGCTGGGAACTTGGAAAGCCACGTTTCACTTCATGAGGAGAT 310  
QY 261 CGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 320  
DB 311 CGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 370  
QY 321 TATGCGGCGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 380  
DB 371 TATGCGGCGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 430  
QY 381 TACTGCAAGAAGACAGCAATGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 431  
DB 431 TACTGCAAGAAGACAGCAATGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 490  
QY 432 -----GGTA 435  
DB 491 CCCTGAGGGCGCTGCGCTGTCCTCCACGTCGCTCTCTCTCTCTCTCTCTCTCTCT 550  
QY 436 GGAATCTCTATACCAACCGGAGGCGCTTGAAGAATTTAAGAATTTGTCGACGCAAG 495  
DB 551 GGAATCTCTATACCAACCGGAGGCGCTTGAAGAATTTAAGAATTTGTCGACGCAAG 610  
QY 496 GACTCTCTGAGAGAGCAATTTTCAAGCCCTCTGACAGCGGAGCTGCTTCCCGAAGCT 555  
DB 611 GACTCTCTGAGAGAGCAATTTTCAAGCCCTCTGACAGCGGAGCTGCTTCCCGAAGCT 670  
QY 556 AGCGAGCGCCCGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 615  
DB 671 AGCGAGCGCCCGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 730  
QY 616 CACTGTGAGCTTACCTTCCAGCGCAAGACCTTCTCTCTCTCTCTCTCTCTCTCTCT 666  
DB 731 CACTGTGAGCTTACCTTCCAGCGCAATGACCTTCTCTCTCTCTCTCTCTCTCTCT 781

Search completed: February 9, 2003, 22:02:23  
Job time : 259.241 secs



Db 421 GCGCTGGAAGAAATTAAGAAATGGTGGAGGCGCAAGGAGCTCTCGGAGGAGACATTTTC 480  
 QY 519 AGGCCCCCTGCAGACGGGAAGCTGGTTCCTCCGGAACAC 554  
 Db 481 AGGCCCCCTGCAGACGGGAAGCTGGTTCCTCCGGAACAC 516

RESULT 3

US-09-614-022-1  
 ; Sequence 1, Application US/09614022  
 ; Patent No. 6165716  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Coriell, Darrrell C.  
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 ; FILE REFERENCE: 97-24  
 ; CURRENT APPLICATION NUMBER: US/09/614,022  
 ; CURRENT FILING DATE: 2000-07-11  
 ; PRIOR APPLICATION NUMBER: 09/130,663  
 ; PRIOR FILING DATE: 1998-08-06  
 ; PRIOR APPLICATION NUMBER: 60/054,867  
 ; PRIOR FILING DATE: 1997-08-06  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 522  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (7)...(516)  
 ; PS-09-614-022-1

Query Match 74.3%; Score 514.4; DB 4; Length 522;  
 Best Local Similarity 99.8%; Pred. No. 1,1e-125;  
 Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 CTGGAGATGAAGACCCCTGTTCTGGGTGTACGCTGGGCTGGCGCTGGCGCTGGCTTCCTTC 98  
 Db 1 CTGGAGATGAAGACCCCTGTTCTGGGTGTACGCTGGGCTGGCGCTGGCGCTGGCTTCCTTC 60  
 QY 99 ACCCTGGAGGAGGAGATATCATCAGGAGACCTGTTACGTAGAGGACCATGTTGTTGTTATAG 158  
 Db 61 ACCCTGGAGGAGGAGATATCATCAGGAGACCTGTTACGTAGAGGACCATGTTGTTGTTATAG 120  
 QY 159 GACTTTCCGGAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
 Db 121 GACTTTCCGGAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 QY 219 GGTGGAGAGTTGGAAGCCACGCTTACCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278  
 Db 181 GGTGGAGAGTTGGAAGCCACGCTTACCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
 QY 279 ATCTGTATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338  
 Db 241 ATCTGTATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 QY 339 ATGTACTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
 Db 301 ATGTACTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 399 CATGGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAATTTGTATACCAACCGGGAG 458  
 Db 361 CATGGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAATTTGTATACCAACCGGGAG 420  
 QY 459 GCGCTGGAAGAAATTAAGAAATTTGGTGCAGCGCAAGGAGCTCTCGGAGGAGGAGGAGGAGGAG 518  
 Db 421 GCGCTGGAAGAAATTAAGAAATTTGGTGCAGCGCAAGGAGCTCTCGGAGGAGGAGGAGGAGGAG 480  
 QY 519 AGGCCCCCTGCAGACGGGAAGCTGGTTCCTCCGGAACAC 554  
 Db 481 AGGCCCCCTGCAGACGGGAAGCTGGTTCCTCCGGAACAC 516

QY 399 CATGGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAATTTGTATACCAACCGGGAG 458  
 Db 361 CATGGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAATTTGTATACCAACCGGGAG 420  
 QY 459 GCGCTGGAAGAAATTAAGAAATTTGGTGCAGCGCAAGGAGCTCTCGGAGGAGGAGGAGGAG 518  
 Db 421 GCGCTGGAAGAAATTAAGAAATTTGGTGCAGCGCAAGGAGCTCTCGGAGGAGGAGGAGGAG 480  
 QY 519 AGGCCCCCTGCAGACGGGAAGCTGGTTCCTCCGGAACAC 554  
 Db 481 AGGCCCCCTGCAGACGGGAAGCTGGTTCCTCCGGAACAC 516

RESULT 2

US-09-432-335-1  
 ; Sequence 1, Application US/09432335  
 ; Patent No. 6143720  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Coriell, Darrrell C.  
 ; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
 ; FILE REFERENCE: 97-24  
 ; CURRENT APPLICATION NUMBER: US/09/432,335  
 ; CURRENT FILING DATE: 1999-11-02  
 ; PRIOR APPLICATION NUMBER: 09/130,663  
 ; PRIOR FILING DATE: 1998-08-06  
 ; PRIOR APPLICATION NUMBER: 60/054,867  
 ; PRIOR FILING DATE: 1997-08-06  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 522  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (7)...(516)  
 ; US-09-432-335-1

Query Match 74.3%; Score 514.4; DB 3; Length 522;  
 Best Local Similarity 99.8%; Pred. No. 1,1e-125;  
 Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 CTGGAGATGAAGACCCCTGTTCTGGGTGTACGCTGGGCTGGCGCTGGCGCTGGCTTCCTTC 98  
 Db 1 CTGGAGATGAAGACCCCTGTTCTGGGTGTACGCTGGGCTGGCGCTGGCGCTGGCTTCCTTC 60  
 QY 99 ACCCTGGAGGAGGAGATATCATCAGGAGACCTGTTACGTAGAGGACCATGTTGTTGTTATAG 158  
 Db 61 ACCCTGGAGGAGGAGATATCATCAGGAGACCTGTTACGTAGAGGACCATGTTGTTGTTATAG 120  
 QY 159 GACTTTCCGGAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
 Db 121 GACTTTCCGGAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 QY 219 GGTGGAGAGTTGGAAGCCACGCTTACCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278  
 Db 181 GGTGGAGAGTTGGAAGCCACGCTTACCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
 QY 279 ATCTGTATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338  
 Db 241 ATCTGTATGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 QY 339 ATGTACTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
 Db 301 ATGTACTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 399 CATGGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAATTTGTATACCAACCGGGAG 458  
 Db 361 CATGGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAATTTGTATACCAACCGGGAG 420  
 QY 459 GCGCTGGAAGAAATTAAGAAATTTGGTGCAGCGCAAGGAGCTCTCGGAGGAGGAGGAGGAGGAG 518





[illegible]

RESULT 9  
 US-08-491-861A-1  
 Sequence 1, Application US/08491861A  
 Patent No. 593283  
 GENERAL INFORMATION:  
 APPLICANT: Morgenstern, Jay P.  
 APPLICANT: Kanieczny, Andrey  
 APPLICANT: Bizindakous, Christine B.  
 APPLICANT: Brauer, Andrew W.  
 TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 TITLE OF INVENTION: Dander and Uses Thereof  
 NUMBER OF SEQUENCES: 104  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII-text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/491.861A  
 FILING DATE: 27-OCT-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/999,712  
 FILING DATE: 31-Dec-92  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Maund-agouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: IMT-0266P(1P-048CP)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 525 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

DB 412 GAGCAGAGCCAGAGGCGCTTGAGGATTTTCGGGAAATCTCAAGAGCCCAAGGA---TTG 468

QY 504 GAGGAGAGCAATTTTCAGCGCCCTTCAGAGCGGGAAGTCGCTTCCGA 551

516

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1 RESULT 8
2 US-08-466-793-1
3 Sequence 1, Application US/08466793
4 Patent No. 5891716
5 GENERAL INFORMATION:
6 APPLICANT: Morgenstern, Jay P.
7 APPLICANT: Kanielszny, Andrzej
8 APPLICANT: Biziadukas, Christine B.
9 APPLICANT: Brauer, Andrew W.
10 TITLE OF INVENTION: Allergenic Proteins and
11 TITLE OF INVENTION: Peptides from Dog
12 TITLE OF INVENTION: Dander and Uses Therefor
13 NUMBER OF SEQUENCES: 104

```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,793  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156,549  
FILING DATE: 22-NOV-1993  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: TMI-0260

```

TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SKO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TTP: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TTP: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..525
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 79..525
US-08-466-793-1

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|    | Query Match           | 21.08;                                                        | Score 145.2;     | DB. 2;          | Length 525; |
|----|-----------------------|---------------------------------------------------------------|------------------|-----------------|-------------|
|    | Best Local Similarity | 60.0%;                                                        | Pred. N. 3.e-29; |                 |             |
|    | Matches 281;          | Conservative                                                  | 0;               | Mismatches 178; | Gaps 9;     |
| QY | 84                    | GCTGCCCTTCCTCACCCGAGAGAGAGATATACAGGACACTGTGAGTGAAGGCC         | 143              |                 |             |
|    |                       |                                                               |                  |                 |             |
|    |                       |                                                               |                  |                 |             |
|    |                       |                                                               |                  |                 |             |
| Dd | 58                    | GATACCCCACCCTCGGAAAGGACACTGTGGCTGTGTGAGGAAATGATNCTGAAGCC      | 117              |                 |             |
|    |                       |                                                               |                  |                 |             |
| QY | 144                   | ATGGTGTCGATAAGAACATTTCCGAGGAGCAGCAGAGGCCCCAGGAGGTGTCCCACTGAAG | 203              |                 |             |



[illegible]

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RESULT 13
US-09-130-663-24
? Sequence 24, Application US/09130663A
? Patent No. 6020163
? GENERAL INFORMATION:
? APPLICANT: Conklin, Darrell C.
? TITLE OF INVENTION: LIPOCALIN HOMOLOG
? FILE REFERENCE: 97-24
? CURRENT APPLICATION NUMBER: US/09/130.663A
? CURRENT FILING DATE: 1998-08-05
? EARLIER APPLICATION NUMBER: 60/054,867
? EARLIER FILING DATE: 1997-08-06
? NUMBER OF SEQ ID NOS: 30
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 24
? LENGTH: 147
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: N-terminal Flag linker
US-09-130-663-24

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|    | Query Match           | 11.08;                                                       | Score 76.2;        | DB 3;     | Length 147; |
|----|-----------------------|--------------------------------------------------------------|--------------------|-----------|-------------|
|    | Best Local Similarity | 96.38;                                                       | Pred. No. 3.1e-11; |           |             |
|    | Matches 78;           | Conservative 0;                                              | Mismatches 3;      | Indels 0; | Gaps 0;     |
| QY | 84                    | GTCCCTCTGCTCTTCCACCTCTGGAGGAGGAGATATACACAGGACCTGCTAGCTGAAGCC | 143                |           |             |
| DY | 67                    | GTCTGCTCTCTTCTTCCCTCCCTGGAGGAGGAGATATACAGGACCTGCTAGCTGAAGCC  | 126                |           |             |
| QY | 144                   | ATGCTGTGTCGATATACAGGACCTTT                                   | 164                |           |             |
| DY | 127                   | ATGCTGTGTCGATATACAGGACCTTT                                   | 147                |           |             |

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RESULT 14
US-09-432-335-24
? Sequence 24, Application US/09432335
? Patent NO. 6143720
? GENERAL INFORMATION:
? APPLICANT: Cogkila, Darrell C.
? TITLE OF INVENTION: LIPOCALIN HOMOLOG
? FILE REFERENCE: 97-24
? CURRENT APPLICATION NUMBER: US/09/432.335
? CURRENT FILING DATE: 1999-11-02
? EARLIER APPLICATION NUMBER: 09/130.663
? EARLIER FILING DATE: 1998-08-06
? EARLIER APPLICATION NUMBER: 60/054.867
? EARLIER FILING DATE: 1997-08-06
? NUMBER OF SEQ ID NOS: 30
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 24
? LENGTH: 147
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURES:
? OTHER INFORMATION: N-terminal Flag linker
US-09-432-335-24

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Query Match 11.0%; Score 76.2; DB 3; Length 147;  
Best Local Similarity 96.3%; Pred. No. 3,le-11;  
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

84 GTCGCCCTGTCCTTCACCTGSGAGGAGGATATCACAGGCACTGTGACGTCAAGCC 143

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Db | 67  | GTGTCTCTTCCTTCACCTCTGAGGAGGAGGATATCACAGGACCTGTGTACTGTGAAGGCC | 146 |
| QY | 144 | ATCTGGTTCGATAAGGACTTT                                        | 164 |
| Db | 127 | ATGTGTTCGATAAAGGACTTT                                        | 147 |

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RESULT 15
08-09-614-022-24
? Sequence 24, Application US/09614022
? Patent No. 6365716
? GENERAL INFORMATION:
? APPLICANT: Cooklib, Darrell C.
? TITLE OF INVENTION: LIPOCALIN HOMOLOG
? FILE REFERENCE: 97-24
? CURRENT APPLICATION NUMBER: US/09/614,022
? CURRENT FILING DATE: 2000-07-11
? PRIOR APPLICATION NUMBER: 09/130,663
? PRIOR FILING DATE: 1998-08-06
? PRIOR APPLICATION NUMBER: 60/054,867
? PRIOR FILING DATE: 1997-08-06
? NUMBER OF SEQ ID NOS: 30
? SOFTWARE: Fastseq for Windows Version 3.0
? SEQ ID NO 24
? LENGTH: 147
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: N-terminal Flag linker
US-09-614-022-24

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|    | Query Match           | 11.08;                                                   | Score 76.2;        | DB 4;     | Length 147; |
|----|-----------------------|----------------------------------------------------------|--------------------|-----------|-------------|
|    | Best Local Similarity | 96.3%;                                                   | Pred. NO. 3.1e-11; |           |             |
|    | Matches 76;           | Conservative 0;                                          | Mismatches 3;      | Indels 0; | Gaps 0;     |
| QY | 84                    | GTCGCTGTCCTTCACCTCGAGGAGGAGATATACACAGGAGCTCGTACGTGAAGGCC | 143                |           |             |
|    |                       |                                                          |                    |           |             |
| Db | 67                    | GTCGTGCTGTCCTTCACCTCGAGGAGGAGATATACAGGAGCTCGTACGTGAAGGCC | 126                |           |             |
|    |                       |                                                          |                    |           |             |
| QY | 144                   | ATGCTGTCGTGATAAGGACTTTT                                  | 164                |           |             |
|    |                       |                                                          |                    |           |             |
| Db | 127                   | ATGCTGTCGTGATAAGGACTTTT                                  | 147                |           |             |
|    |                       |                                                          |                    |           |             |

Search completed: February 9, 2003, 22:05:18  
Job time : 55.2996 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 21:14:50 ; Search time 53.348 Seconds  
(without alignments)  
6148.496 Million cell updates/sec

Title: US-09-099-823-4  
Perfect score: 692  
Sequence: 1 GAGCCGACGACCTGCGGA.....ATTAAGTCCTTCGCCCA 692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues  
Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications.NR.\*  
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2: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubna/US08\_NEW\_PUB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*  
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12: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Query | Score | Match | Length | DB ID              | Description        |
|------------|-------|-------|-------|--------|--------------------|--------------------|
| 1          | 692   | 100.0 | 692   | 10     | US-09-099-823-4    | Sequence 4, Appl   |
| 2          | 692   | 100.0 | 692   | 10     | US-09-099-823-5    | Sequence 5, Appl   |
| 3          | 514.4 | 74.3  | 523   | 10     | US-09-951-845-1    | Sequence 1, Appl   |
| c 4        | 483.6 | 69.9  | 501   | 10     | US-09-833-381-803  | Sequence 803, Appl |
| c 5        | 337   | 48.7  | 337   | 10     | US-09-099-823-3    | Sequence 3, Appl   |
| 6          | 296   | 42.8  | 336   | 10     | US-09-833-381-1747 | Sequence 1747, Ap  |
| 7          | 245   | 35.4  | 245   | 10     | US-09-099-823-2    | Sequence 2, Appl   |
| 8          | 236   | 34.1  | 236   | 10     | US-09-099-823-1    | Sequence 1, Appl   |
| 9          | 145.2 | 21.0  | 525   | 10     | US-09-374-571-1    | Sequence 1, Appl   |
| 10         | 54.8  | 7.9   | 555   | 9      | US-10-143-576-1    | Sequence 9, Appl   |
| 11         | 54.8  | 7.9   | 555   | 10     | US-09-854-847-9    | Sequence 9, Appl   |
| 12         | 54.8  | 7.9   | 579   | 10     | US-09-854-847-17   | Sequence 17, Appl  |
| 13         | 53.2  | 7.7   | 762   | 9      | US-10-028-072-237  | Sequence 237, App  |
| 14         | 53.2  | 7.7   | 762   | 9      | US-10-121-049-237  | Sequence 237, App  |
| 15         | 53.2  | 7.7   | 762   | 9      | US-10-123-904-237  | Sequence 237, App  |
| 16         | 53.2  | 7.7   | 762   | 9      | US-10-140-470-237  | Sequence 237, App  |
| 17         | 53.2  | 7.7   | 762   | 9      | US-09-854-847-25   | Sequence 25, Appl  |
| 18         | 48    | 6.9   | 432   | 10     | US-09-854-847-25   | Sequence 25, Appl  |
| 19         | 46    | 6.6   | 570   | 10     | US-09-800-729-37   | Sequence 37, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-099-823-4  
; Sequence 4, Application US/09099823  
; Patent No. US20020018990A1  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRAMADOS, EDWARD N.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KASS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: SCHEFFEL, CHRISTI  
; APPLICANT: STROUPE, STEPHEN D.  
; APPLICANT: YU, HONG  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/09/099,823  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/879,354  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.

|      |      |     |      |    |                     |                   |
|------|------|-----|------|----|---------------------|-------------------|
| c 20 | 40   | 5.8 | 948  | 10 | US-09-886-055-194   | Sequence 194, App |
| 21   | 38.2 | 5.5 | 264  | 10 | US-09-878-574-11281 | Sequence 11281, A |
| 22   | 38.2 | 5.5 | 299  | 10 | US-09-878-574-11878 | Sequence 11878, A |
| 23   | 38.2 | 5.5 | 385  | 10 | US-09-878-574-59    | Sequence 59, Appl |
| 24   | 38.2 | 5.5 | 391  | 10 | US-09-878-574-2305  | Sequence 2305, Ap |
| 25   | 38.2 | 5.5 | 504  | 10 | US-09-878-574-4330  | Sequence 4330, Ap |
| 26   | 38.2 | 5.5 | 1914 | 10 | US-09-815-242-7960  | Sequence 7960, Ap |
| 27   | 37.6 | 5.4 | 1852 | 10 | US-09-969-852-4     | Sequence 4, Appl  |
| c 28 | 36.8 | 5.3 | 576  | 9  | US-09-938-842A-1855 | Sequence 1855, Ap |
| 29   | 36.6 | 5.3 | 320  | 10 | US-09-923-875-3670  | Sequence 3670, Ap |
| 30   | 36.4 | 5.3 | 2602 | 10 | US-09-917-800A-1590 | Sequence 1590, Ap |
| 31   | 36.2 | 5.2 | 3502 | 10 | US-09-880-192-37    | Sequence 37, Appl |
| c 32 | 36   | 5.2 | 1464 | 9  | US-10-166-359-1     | Sequence 1, Appl  |
| c 33 | 36   | 5.2 | 1464 | 9  | US-10-166-113-1     | Sequence 1, Appl  |
| c 34 | 36   | 5.2 | 1464 | 9  | US-10-166-357-1     | Sequence 1, Appl  |
| c 35 | 36   | 5.2 | 1464 | 9  | US-10-166-372-1     | Sequence 1, Appl  |
| c 36 | 36   | 5.2 | 1464 | 10 | US-09-149-045-1     | Sequence 1, Appl  |
| 37   | 36   | 5.2 | 5513 | 10 | US-09-751-1008-98   | Sequence 98, Appl |
| 38   | 35.8 | 5.2 | 2379 | 10 | US-09-815-242-7868  | Sequence 7868, Ap |
| c 39 | 35.8 | 5.2 | 3698 | 9  | US-09-945-901-43    | Sequence 43, Appl |
| c 40 | 35.8 | 5.2 | 3698 | 9  | US-10-007-747-43    | Sequence 43, Appl |
| c 41 | 35.8 | 5.2 | 3698 | 9  | US-10-038-937-43    | Sequence 53, Appl |
| c 42 | 35.8 | 5.2 | 4002 | 9  | US-09-945-901-53    | Sequence 53, Appl |
| c 43 | 35.8 | 5.2 | 4002 | 9  | US-10-007-747-53    | Sequence 53, Appl |
| c 44 | 35.8 | 5.2 | 4002 | 9  | US-10-038-937-53    | Sequence 53, Appl |
| c 45 | 35.8 | 5.2 | 4017 | 9  | US-09-945-901-49    | Sequence 49, Appl |



Mon Feb 10 11:11:58 2003

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QY 301 AGCTTGGCAATACAGAGCCCTATGGGGGAGGAGCTCATGTACCTGAGAGAGTGGCCA 360
Db 301 AGCTTGGCAATACAGAGCCCTATGGGGGAGGAGCTCATGTACCTGAGAGAGTGGCCA 360
QY 361 GGAGGGACCACTACATCTTTTACTGCAAGACACAGACACCATGGGGGCTGCTCCACATGG 420
Db 361 GGAGGGACCACTACATCTTTTACTGCAAGACACAGACACCATGGGGGCTGCTCCACATGG 420
QY 421 GAACCTTGGGTAGAGATCTGTATACCAACCGGGAGGCTTGGAGAGATTTAAGAAAT 480
Db 421 GAACCTTGGGTAGAGATCTGTATACCAACCGGGAGGCTTGGAGAGATTTAAGAAAT 480
QY 481 TGGTGCAGCCAGAGGACTCTGGAGAGAGACATTTTACGCCCCCTGACAGCGGAGCT 540
Db 481 TGGTGCAGCCAGAGGACTCTGGAGAGAGACATTTTACGCCCCCTGACAGCGGAGCT 540
QY 541 GGGTTCCGGAACACTAGGAGCCCCCGGGGCTGACCTCCAGAGCCACCTTACCCAG 600
Db 541 GGGTTCCGGAACACTAGGAGCCCCCGGGGCTGACCTCCAGAGCCACCTTACCCAG 600
QY 601 ACACAGAGCCGAGACCTGGAGACCTACCTCCAGCATGACCTTCCCTGCTCCACCC 660
Db 601 ACACAGAGCCGAGACCTGGAGACCTACCTCCAGCATGACCTTCCCTGCTCCACCC 660
QY 661 ACCTGACCTCAATTAAGTCTTCTCCGCCCA 692
Db 661 ACCTGACCTCAATTAAGTCTTCTCCGCCCA 692

RESULT 3
US-09-951-845-1
; Sequence 1, Application US/09951845
; Patent No. US20020098497A1
; GENERAL INFORMATION:
; APPLICANT: Lok, SI
; APPLICANT: Foster, Donald C.
; APPLICANT: Holloway, James L.
; TITLE OF INVENTION: Use of Human Pheromone Polypeptides
; FILE REFERENCE: 00-85
; CURRENT APPLICATION NUMBER: US/09/951,845
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (8)...(517)
US-09-951-845-1

Query Match 74.3%; Score 514.4; DB 10; Length 523;
Best Local Similarity 99.8%; Pred. No. 1.1e-126; Indels 0; Gaps 0;
Matches 515; Conservative 0; Mismatches 1;

QY 39 CTGGAGATGAAGACCTCTCTGGGTGTCAAGCTGGCTGGCGCTGGCGCTGCTCTTC 98
Db 2 CTGAGATGAAGACCTCTCTGGGTGTCAAGCTGGCTGGCGCTGGCGCTGCTCTTC 61

QY 99 ACCCTGGAGAGGAGATATACAGGAGCTGTGTAGTGAAGGCCATGGTGGTGCAGTAAG 158
Db 62 ACCCTGGAGAGGAGATATACAGGAGCTGTGTAGTGAAGGCCATGGTGGTGCAGTAAG 121

QY 159 GACTTTCGGAG 218
Db 122 GACTTTCGGAG 181

QY 219 GGTGGAGAGTTGGAG 278
Db 182 GGTGGAGAGTTGGAG 241
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QY 279 ATCTGTATGCGGAG 338
Db 242 ATCTGTATGCGGAG 301
QY 339 ATGTACTCTGAGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 398
Db 302 ATGTACTCTGAGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
QY 399 CATGGGGGCTCTCCATATGAGGAAAGCTGTGGTGGTGGTGGTGGTGGTGGTGG 458
Db 362 CATGGGGGCTCTCCATATGAGGAAAGCTGTGGTGGTGGTGGTGGTGGTGGTGG 421
QY 459 GCGCTTGGAGAAATTTAAGAAATTTGTCAGCGCAAGGAGACTCTCGAGGAGAG 518
Db 422 GCGCTTGGAGAAATTTAAGAAATTTGTCAGCGCAAGGAGACTCTCGAGGAGAG 481
QY 519 AGCCCTCTGAG 554
Db 482 AGCCCTCTGAG 517

RESULT 4
US-09-833-381-803/c
; Sequence 803, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-803

Query Match 69.9%; Score 483.6; DB 10; Length 501;
Best Local Similarity 99.0%; Pred. No. 1.5e-116; Indels 1; Gaps 1;
Matches 497; Conservative 0; Mismatches 4;

QY 189 GTGTCCCGAGTGAAGTGCAGAGCCCTGGCGGTGGGAGTGTGGAAGTGTGACCTTC 248
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QY 249 ATGAGGAGAGATCGGTGCATCCAGAGAAATCTGTATGCGGAGAGAGAGAGAGAG 308
Db 442 ATGAGGAGAGATAGGTGCATCCAGAGAAATCTGTATGCGGAGAGAGAGAGAGAG 383

QY 309 AATATAGCGCTATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
Db 382 AATATAGCGCTATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323

QY 369 CACTACATCTTTTACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428
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QY 429 GTGGTGGAGAAATTTGATATCCAAACCGGGAGGCGCTTGGAGAAATTTAAGAAAT 488
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Db 202 CGCAAGGAG 143

QY 549 GAGACATAGGAG 608
Db 142 GAGACATAGGAG 83
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Db 82 CCGGACCACTGGACCTACCTCCAGCCATGACCTTCCTGCTCCACCCACCTGACT 23  
QY 669 CCAATTAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 690  
Db 22 CCAATTAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1

RESULT 5  
US-09-099-823-3/c  
; Sequence 3, Application US/09099823  
; Patent No. US20020018990A1  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: SCHEFFEL, CHRISTI  
; APPLICANT: STROUD, STEPHEN D.  
; APPLICANT: YU, HONG  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/099,823  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/879,354  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6120.US.PI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 337 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-099-823-3

Query Match 48.7%; Score 337; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 6.2e-80;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 354 CTGCCCCAGGAGGACCACTACATCTTTTACTGCAAGACACACACCATGGGGGCTGCTC 413  
Db 337 CTGCCCCAGGAGGACCACTACATCTTTTACTGCAAGACACACACCATGGGGGCTGCTC 278

QY 414 CACATGGGAAGCTTGTGGTAGGAATTCGTATACCAACCGGAGGCGCTTGGAGAATTT 473  
Db 277 CACATGGGAAGCTTGTGGTAGGAATTCGTATACCAACCGGAGGCGCTTGGAGAATTT 218  
QY 474 AAGAAATTTGTGACCCCAAGGAGCTCTCGGAGGAGGACATTTTCAGCCCTTCAGAG 533  
Db 217 AAGAAATTTGTGACCCCAAGGAGCTCTCGGAGGAGGACATTTTCAGCCCTTCAGAG 158  
QY 534 GGAAGTGTCTTCCGCAACACTAGGACAGCCCTCGGCTCTGCACTTCCAGAGCCACCTA 593  
Db 157 GGAAGTGTCTTCCGCAACACTAGGACAGCCCTCGGCTCTGCACTTCCAGAGCCACCTA 98  
QY 594 CCACACAGACAGAGCCCGGACCACTCTGGACCTACCTCCAGCCATGACCTTCCCTGCT 653  
Db 97 CCACACAGACAGAGCCCGGACCACTCTGGACCTACCTCCAGCCATGACCTTCCCTGCT 38  
QY 654 CCACACCACTGACTCTCCAAATAAGTCTTCTCTCCCC 690  
Db 37 CCACACCACTGACTCTCCAAATAAGTCTTCTCTCCCC 1

RESULT 6  
US-09-833-381-1747  
; Sequence 1747, Application US/09833381  
; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; PRIOR APPLICATION NUMBER: 2001-04-11  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1747  
; LENGTH: 336  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-833-381-1747

Query Match 42.8%; Score 296; DB 10; Length 336;  
Best Local Similarity 99.4%; Pred. No. 4.1e-69;  
Matches 318; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
QY 2 AGCCCCAGTGACCTGCGGAGGTCGCGAGACAGAGCTCTGGAGATGAGACCTGTTCCT 61  
Db 17 AGCCCCAGTGACCTGCGGAGGTCGCGAGACAGAGCTCTGGAGATGAGACCTGTTCCT 76  
QY 62 GGGTGTCACTGCGGCTGCGGCTGCGCTTGTCTTCACTTCCCTTGGAGAGGAGATATCAC 121  
Db 77 GGGTGTCACTGCGGCTGCGGCTGCGCTTGTCTTCACTTCCCTTGGAGAGGAGATATCAC 136  
QY 122 AGGGACCTTGTA-CGTGAAGGCCATGCTGCTGATATAGGACTTTCGGAGGACAGAGGC 180  
Db 137 AGGGACCTTGTA-CGTGAAGGCCATGCTGCTGATATAGGACTTTCGGAGGACAGAGGC 196  
QY 181 CCAGGAAGTGTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240  
Db 197 CCAGGAAGTGTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 256  
QY 241 TCACCTTTCATGAGGAGGATCGGTGCTATCCAGAGAAATCTCTGATG-CGGAAGCGAG 299  
Db 257 TCACCTTTCATGAGGAGGATCGGTGCTATCCAGAGAAATCTCTGATG-CGGAAGCGAG 316  
QY 300 GAGCTGCGCAATATACAGCC 319  
Db 317 GAGCTGCGCAATATACAGCC 336

RESULT 7  
US-09-099-823-2  
; Sequence 2, Application US/0909823

Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120.US.P1  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-099-823-2  
Query Match 35.4%; Score 245; DB 10; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.1e-55;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 113 GGATATACAGAGGACCTGTACGTGAGAGCCATGCTGCTGATAGAGACTTTCGGAGGA 172  
DB 1 GGATATACAGAGGACCTGTGATGAGAGCCATGCTGCTGATAGAGACTTTCGGAGGA 60  
QY 173 CAGGAGGCCAGAGAGGTGTCCCAAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGA 232  
DB 61 CAGGAGGCCAGAGAGGTGTCCCAAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGA 120  
QY 233 AGCCAGCTTACCTTCATGAGGAGGATCGGTGCATCCAGAGAAAATCCTGATGCGGAA 292  
DB 121 AGCCAGCTTACCTTCATGAGGAGGATCGGTGCATCCAGAGAAAATCCTGATGCGGAA 180  
QY 293 GACGAGGAGCTTGGCAATACAGCGCTATGGGCGCAGAGAGCTCATGTACTGACGAGA 352  
DB 181 GACGAGGAGCTTGGCAATACAGCGCTATGGGCGCAGAGAGCTCATGTACTGACGAGA 240

QY 353 GCTGC 357  
DB 241 GCTGC 245  
RESULT 8  
US-09-099-823-1  
Sequence 1, Application US/0909823  
Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120.US.P1  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-099-823-1  
Query Match 34.1%; Score 236; DB 10; Length 236;  
Best Local Similarity 100.0%; Pred. No. 2.5e-53;  
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCGCCAGTACCTGCGAGAGGTGGCAGCAGAGCTGTGAGATGAAGACCTGTTC 60  
DB 1 GAGCGCCAGTACCTGCGAGAGGTGGCAGCAGAGCTGTGAGATGAAGACCTGTTC 60  
QY 61 TGGGTGTACGCTGGCGCTGGCCCTGCTTCCCTTACCTGGAGGAGGATATCA 120  
DB 61 TGGGTGTACGCTGGCGCTGGCCCTGCTTCCCTTACCTGGAGGAGGATATCA 120

QY 121 CAGGAGCTGTACGTAGAGGCGATGGTGTGATTAAGGACTTTCCGAGGACAGGAGGC 180  
 Db 121 CAGGAGCTGTACGTAGAGGCGATGGTGTGATTAAGGACTTTCCGAGGACAGGAGGC 180  
 QY 181 CCAGGAGGTGTCCTCCAGTGAAGTGTACAGCCCTGGCGGTGGGAAGTGGAGGCC 236  
 Db 181 CCAGGAGGTGTCCTCCAGTGAAGTGTACAGCCCTGGCGGTGGGAAGTGGAGGCC 236

RESULT 9  
 US-09-374-671-1  
 ; Sequence 1, Application US/09374671  
 ; Patent No. US20020012963A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morgenstern, Jay P.  
 ; APPLICANT: Kalciczny, Andrzej  
 ; APPLICANT: Bizindaukas, Christine B.  
 ; APPLICANT: Brauer, Andrew W.  
 ; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 ; TITLE OF INVENTION: Dander and Uses Therefor  
 ; NUMBER OF SEQUENCES: 104  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 ; STREET: 28 State Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-Text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/374,671  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/491,861  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mandragoras, Amy E.  
 ; REGISTRATION NUMBER: 36,207  
 ; REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 742-4214  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 525 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..525  
 ; FEATURE:  
 ; NAME/KEY: mat.peptide  
 ; LOCATION: 79..525  
 ; US-09-374-671-1

Query Match 21.0%; Score 145.2; DB 10; Length 525;  
 Best Local Similarity 60.0%; Pred. No. 2.9e-29;  
 Matches 281; Conservative 0; Mismatches 178; Indels 9; Gaps 2;  
 QY 84 GTGCGCTGTCTTCACCTTCGAGGAGGAGGATATCACAGGAGCTGTACGTGAGAGGC 143  
 Db 58 GATACCCCGCCCTTGGGAAGGACACTGTGGTGTGTCTCAGGAGGAATGGTATCTGAGGCC 117  
 QY 144 ATGGTGTGTGATTAAGGACTTTCCGAGGACAGAGGCCAGGAAGGTGTCCGCCAGTGAAG 203  
 Db 118 ATGACAGACAGACAGAGGTGCGCTCA-----GAAGCTGACTCACTGACTCCCATGATC 171

QY 204 GTGACAGCCCTGGCGGTGGGAAGTGTGGAAGCCACGCTTCACCTTCAATGAGGAGGATCGG 263  
 Db 172 CTCRAAGCCCGAGAGGGGGCAAACTTGAAGCCAAAGATCACCCTGCTGACAAATGCTGAC 231  
 QY 264 TGCATCCAGAGAAAATCTTGATGCGGAGACGAGGAGGAGCTGGCAAAATACAGCGCTAT 323  
 Db 232 TCCAGAGACATCAGCGTGTCTTGCACAAACCTCTGAGCTGAGCAATACACGGCATAC 291  
 QY 324 GGGGGCAGAGACCTGATGCTGACGAGCTGCCAGGAGGAGGACCATCATCTTTTAC 383  
 Db 292 GAGGCGCAGCGTGTGCTGTTTCATCCAGCGTCCCGGTGAGGAGACCATCATCTTTTAC 351  
 QY 384 TCAAGACAGCAGCAGCATGAGGGGCTGCTCCATATGGAAGAGCTTGTGGTAGGAATCT 443  
 Db 352 TCGAGGGCGAGCTCCATGAGGAGCAGATCCGAATGSCCAAGCTTCTGGGAAGGATCT 411  
 QY 444 GATACCAACCGGAGGCGCTTGAAGAAATTTAAGAAATTTGTCAGCGCAAGGAGCTCTCG 503  
 Db 412 GAGCAGAGCAAGAGGCGCTTGGAGGAATTTTCGGGAATTTCTCAAGAGCCAAAGGA--TTG 468  
 QY 504 GAGGAGACATTTTCAAGCGCTTGCAGCGGGAAGCTGGTTCGCCGA 551  
 Db 469 RACCAGAGATTTTGAAGCTGCCGAGAGGAAACCTGCTCTCCAGGA 516

RESULT 10  
 US-10-143-576-1  
 ; Sequence 1, Application US/10143576  
 ; Publication No. US20030013151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HU, Song et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
 ; TITLE OF INVENTION: USES THEREOF  
 ; FILE REFERENCE: CL001237  
 ; CURRENT APPLICATION NUMBER: US/10/143,576  
 ; CURRENT FILING DATE: 2002-05-13  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 555  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-143-576-1

Query Match 7.9%; Score 54.8; DB 9; Length 555;  
 Best Local Similarity 46.6%; Pred. No. 2.1e-05;  
 Matches 247; Conservative 0; Mismatches 277; Indels 6; Gaps 2;  
 QY 45 ATGAAGACCTCTTCCTGGGTGTACGCTCGGCGCTGGCGCTGCTGCTTCTTCCCTG 104  
 Db 25 ATCTTGACCTCTCTCTGGGCGCCAGCGGCTCAGGCTGAGGTTCTGCTGAGCCTGACTTC 84  
 QY 105 GAGGAGGAGGATATCACAGGAGCCTGGTACGTGAAGGCCATGG---TGTCGATPAAGGAC 161  
 Db 85 AATGCTGAAAAGTCTCAGGCGCTCTGTTGTTCTTCCATGTCATGTCGACTGAGGCTC 144  
 QY 162 TTTCCGAGGACAGGAGGCGCCAGGAAGGTGTCCCGAGTGAAGGTGACAGCCCTGGCGGT 221  
 Db 145 TTCTGCGAAGAGGAGGACCACTGTCCATGTCCAGAGGCGCATCAGGCCACAGAGGAG 204  
 QY 222 GGAAGTGTGAGACGAGCTTACCTTCATGAGGAGGAGGAGTGGTGCATCCAGAGAAATC 281  
 Db 205 GCGGCGCTTCAGCTCCATGAGGATTCGCGGCGCGAGCGCTGTACACCGAGTGGATGCC 264  
 QY 282 CTGATGCGGAAGACAGGAGGAGGCTTGGCAATAACAGCGCCATFG---GGGGCAGGAAGCTC 338  
 Db 265 GAGTACCTGAGAGTGGGCTCGAGGAGGACACTTCAGAGTCCCGGCGCTTGGGCTACTGGAC 324  
 QY 339 ATGTACCTGAGAGGAGTGGCCAGAGGAGGAGGACCATCATCTTTTACTGCAAGACAGAC 398  
 Db 325 GTGGCATGTCGACACACACTACAGCTCTTCCGCTCTTCTTACATCTACAGAGGAGCTG 384

QY 399 CATGGGGGCTCTCCACATGGGAAAGCTTGTGGTAGGAATTCGTATACCAACCGGGAG 458  
DB 385 GAGGGGGCTCTCAGCACCATTGTGCTACAGCGCGACCCAGGATCTGAGTCCCGCAG 444  
QY 459 GCGCTGAGAGATTTAGAAATTTGTCAGCGCAAGGAGCTCTCGAGGAGGACATTTTC 518  
DB 445 GCTCTGAGGGCTTCCAGGACTTCTACCGGACCTTGGGCTCCCGGAGGACATGATGTC 504  
QY 519 AGGCGCTCGAGCGGAGAGCTGTGCTCCGAACATAGGACAGCCCGG 568  
DB 505 ATGCTGCCCCAGTCAGATCATGCAACCTGAGAGCAAGGAGGCGCCCTG 554

## RESULT 11

US-09-854-847-1  
; Sequence 1, Application US/09854847  
; Patent No. US20020107375A1  
; GENERAL INFORMATION:  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020107375A1el Human Lipocalin Homologs and Polynucleotide  
; FILE REFERENCE: LEX-0173-USA  
; CURRENT APPLICATION NUMBER: US/09/854,847  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/203,874  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-854-847-1

Query Match 7.9%; Score 54.8; DB 10; Length 555;  
Best Local Similarity 46.6%; Pred. No. 2.1e-05;  
Matches 247; Conservative 0; Mismatches 277; Indels 6; Gaps 2;

QY 45 ATGAGAGACCTGTCTCTGGGTGTACAGCTCGGCGCTGGCGCTGCTGCTTCCTTCACCCCTG 104  
DB 25 ATCTGACCTGTCTCTGGGCGCCACAGGCTCAGGCTGAGGTTCGTGCTGACCTGATTC 84  
QY 105 GAGGAGGAGATATACAGGAGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 161  
DB 85 AATGCTGAAGATTTCTCAGGCGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 144  
QY 162 TTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 221  
DB 145 TTCTGGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 204  
QY 222 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 281  
DB 205 GCGGCGCTCCAGCTCCAGTGGAGTTCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 264  
QY 282 CTGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338  
DB 265 GAGTACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 324  
QY 339 ATGTACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
DB 325 GTGCGCATCTGTGACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 384  
QY 399 CATGGGGGCTCTCCACATGGGAAAGCTTGTGGTAGGAATTCGTATACCAACCGGGAG 458  
DB 385 GAGGGGGCTCTCAGCACCATTGTGCTACAGCGCGACCCAGGATCTGAGTCCCGCAG 444  
QY 459 GCGCTGAGAGATTTAGAAATTTGTCAGCGCAAGGAGCTCTCGAGGAGGACATTTTC 518  
DB 445 GCTCTGAGGGCTTCCAGGACTTCTACCGGACCTTGGGCTCCCGGAGGACATGATGTC 504  
QY 519 AGGCGCTCGAGCGGAGAGCTGTGCTCCGAACATAGGACAGCCCGG 568

DB 505 ATGCTGCCCCAGTCAGATCATGCAACCTGAGAGCAAGGAGGCGCCCTG 554

## RESULT 12

US-09-854-847-9  
; Sequence 9, Application US/09854847  
; Patent No. US20020107375A1  
; GENERAL INFORMATION:  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020107375A1el Human Lipocalin Homologs and Polynucleotide  
; FILE REFERENCE: LEX-0173-USA  
; CURRENT APPLICATION NUMBER: US/09/854,847  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/203,874  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 579  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-854-847-9

Query Match 7.9%; Score 54.8; DB 10; Length 579;  
Best Local Similarity 46.6%; Pred. No. 2.1e-05;  
Matches 247; Conservative 0; Mismatches 277; Indels 6; Gaps 2;

QY 45 ATGAGAGACCTGTCTCTGGGTGTACAGCTCGGCGCTGGCGCTGCTGCTTCCTTCACCCCTG 104  
DB 49 ATCTGACCTGTCTCTGGGCGCCACAGGCTCAGGCTGAGGTTCGTGCTGACCTGATTC 108  
QY 105 GAGGAGGAGATATACAGGAGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 161  
DB 109 AATGCTGAAGATTTCTCAGGCGCTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 168  
QY 162 TTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 221  
DB 169 TTCTGGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 228  
QY 222 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 281  
DB 229 GCGGCGCTCCAGCTCCAGTGGAGTTCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288  
QY 282 CTGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338  
DB 289 GAGTACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348  
QY 339 ATGTACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 398  
DB 349 GTGCGCATCTGTGACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408  
QY 399 CATGGGGGCTCTCCACATGGGAAAGCTTGTGGTAGGAATTCGTATACCAACCGGGAG 458  
DB 409 GAGGGGGCTCTCAGCACCATTGTGCTACAGCGCGACCCAGGATCTGAGTCCCGCAG 468  
QY 459 GCGCTGAGAGATTTAGAAATTTGTCAGCGCAAGGAGCTCTCGAGGAGGACATTTTC 518  
DB 469 GCTCTGAGGGCTTCCAGGACTTCTACCGGACCTTGGGCTCCCGGAGGACATGATGTC 528  
QY 519 AGGCGCTCGAGCGGAGAGCTGTGCTCCGAACATAGGACAGCCCGG 568  
DB 529 ATGCTGCCCCAGTCAGATCATGCAACCTGAGAGCAAGGAGGCGCCCTG 578

## RESULT 13

US-09-854-847-17  
; Sequence 17, Application US/09854847  
; Patent No. US20020107375A1  
; GENERAL INFORMATION:  
; APPLICANT: Mathur, Brian  
; TITLE OF INVENTION: No. US20020107375A1el Human Lipocalin Homologs and Polynucleotide









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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:05:30 ; Search time 1923.58 Seconds  
(without alignments)  
5826.269 Million cell updates/sec

Title: US-09-099-823-4  
Perfect score: 692  
Sequence: 1 GAGGCCGACCTGCCGA.....ATTAAGTCTTCTCCGCCCA 692

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapert 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: em\_estha.\*

2: em\_esthum.\*

3: em\_estlin.\*

4: em\_estma.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hic.\*

9: gb\_estl.\*

10: gb\_est2.\*

11: gb\_hic.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pln.\*

21: em\_gss\_vrt.\*

22: em\_gss\_fun.\*

23: em\_gss\_man.\*

24: em\_gss\_mus.\*

25: em\_gss\_othr.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| c 1        | 499   | 72.1        | 532    | 10 AW513637 | AW513637 x047b10.x |
| c 2        | 465   | 67.2        | 513    | 9 AA977608  | AA977608 on61e03.s |
| c 3        | 460.6 | 66.6        | 477    | 9 AI251747  | AI251747 qn09f12.x |
| c 4        | 452.8 | 65.4        | 499    | 9 AI219510  | AI219510 qn24d02.x |
| c 5        | 410.4 | 59.3        | 415    | 9 AA460385  | AA460385 xz51e06.r |
| c 6        | 375   | 54.2        | 431    | 9 AA936288  | AA936288 on75f11.s |

|      |       |      |      |             |                     |
|------|-------|------|------|-------------|---------------------|
| c 7  | 337   | 48.7 | 337  | 9 AA460323  | AA460323 xz51e06.s  |
| c 8  | 329.2 | 47.6 | 349  | 9 AI143970  | AI143970 ge01c11.x  |
| c 9  | 171.2 | 24.7 | 603  | 10 BB618259 | BB618259 BB618259   |
| c 10 | 169.6 | 24.5 | 626  | 10 BB028765 | BB028765 BB028765   |
| c 11 | 162.2 | 23.4 | 519  | 9 AI877465  | AI877465 udl0d09.r  |
| c 12 | 156.4 | 22.6 | 494  | 14 R47029   | R47029 r358 Rat in  |
| c 13 | 148   | 21.4 | 337  | 12 BF193883 | BF193883 245614 MA  |
| c 14 | 146   | 21.1 | 594  | 10 AW020286 | AW020286 ESTF351590 |
| c 15 | 119.8 | 17.3 | 501  | 10 AW049121 | AW049121 UI-M-BHI-  |
| c 16 | 98.4  | 14.2 | 462  | 13 BM087898 | BM087898 500754 MA  |
| c 17 | 82    | 11.8 | 438  | 12 BF603580 | BF603580 269132 MA  |
| c 18 | 55.4  | 8.0  | 518  | 12 BG814151 | BG814151 daf64a03.  |
| c 19 | 53.8  | 7.8  | 312  | 9 AA851021  | AA851021 EST193789  |
| c 20 | 53.4  | 7.7  | 434  | 12 BF403590 | BF403590 UI-R-CAL-  |
| c 21 | 51    | 7.4  | 322  | 12 BF288401 | BF288401 EST452992  |
| c 22 | 50.8  | 7.3  | 513  | 12 BF403655 | BF403655 UI-R-CAL-  |
| c 23 | 48.4  | 7.0  | 521  | 12 BF404046 | BF404046 Tetraodon  |
| c 24 | 47.6  | 6.9  | 1020 | 17 CNS03858 | AL256805 Tetraodon  |
| c 25 | 47.4  | 6.8  | 426  | 10 AW158517 | AW158517 za42c10.x  |
| c 26 | 46.4  | 6.7  | 571  | 12 BF396144 | BF396144 UI-R-CAL-  |
| c 27 | 46.4  | 6.6  | 758  | 17 BH359934 | BH359934 CH230-126  |
| c 28 | 45.8  | 6.6  | 618  | 13 BJ045011 | BJ045011 BJ045011   |
| c 29 | 45.4  | 6.6  | 618  | 13 BJ045011 | BJ045011 BJ045011   |
| c 30 | 45.2  | 6.5  | 742  | 13 BI520644 | BI520644 166614 BA  |
| c 31 | 45    | 6.5  | 742  | 13 BI520644 | BI520644 603071606  |
| c 32 | 44.6  | 6.4  | 494  | 14 BQ032434 | BQ032434 UI-I-CFO-  |
| c 33 | 44.4  | 6.4  | 910  | 17 CNS0060N | AL065629 Drosophila |
| c 34 | 44.2  | 6.4  | 339  | 14 BQ461044 | BQ461044 HEU1601r   |
| c 35 | 44.2  | 6.4  | 417  | 14 N68123   | N68123 YZ54611.s1   |
| c 36 | 44.2  | 6.4  | 551  | 14 BQ469025 | BQ469025 HM03C09r   |
| c 37 | 44.2  | 6.4  | 576  | 14 BQ463781 | BQ463781 HG01G16r   |
| c 38 | 44.2  | 6.4  | 647  | 13 BI954086 | BI954086 HVSMM001   |
| c 39 | 44.2  | 6.4  | 663  | 13 BI957662 | BI957662 HVSMM001   |
| c 40 | 44.2  | 6.4  | 805  | 12 BF267509 | BF267509 HV.Cha001  |
| c 41 | 44.2  | 6.4  | 820  | 12 BF265032 | BF265032 HV.Cha001  |
| c 42 | 44.2  | 6.4  | 847  | 13 BI953660 | BI953660 HVSMM001   |
| c 43 | 44.2  | 6.4  | 875  | 12 BF267309 | BF267309 HV.Cha001  |
| c 44 | 44    | 6.4  | 538  | 9 AL588422  | AL588422 AL588422   |
| c 45 | 44    | 6.4  | 581  | 9 AL588768  | AL588768 AL588768   |

ALIGNMENTS

RESULT 1  
AW513637/c  
LOCUS  
DEFINITION  
x047b10.x1 NCI CGAP Utl Homo sapiens CDNA clone IMAGE:2707171 3', similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. ;, mRNA sequence.  
ACCESSION  
AW513637  
VERSION  
AW513637.1  
KEYWORDS  
EST  
SOURCE  
human  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 532)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
TITLE  
Unpublished (1997)  
JOURNAL  
Contact: Robert Strausberg, Ph.D.  
COMMENT  
Email: cgapsb-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILMUG at: [image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 316.

**FEATURES**

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location/qualifiers
1. 532
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2707171"
/clone_lib="NCI_CGAP_Ut1"
/tissue_type="well-differ
adenocarcinoma, 7 pooled
```

| II538-014 <sup>a</sup> |          |       |          |
|------------------------|----------|-------|----------|
| BASE COUNT             | 87 a     | 145 c | 159 g    |
| ORIGIN                 | 2 others | 139 t | 2 others |

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Query Match 72.1%; Score 499; DB 10; Length 532;
Best Local Similarity 96.8%; pred. NO. 2.6e-110;
Matches 508; Conservative 0; Mismatches 17; Indels 0; Gaps 0
```

[illegible]

| RESULT 2 | AA977608/c | LOCUS | DEFINITION |
|----------|------------|-------|------------|
|----------|------------|-------|------------|

AA977608 513 bp mRNA linear EST 26-ADG-1998  
on61ed03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1561180 3' similar to TR:Q63613 Q63613 ODORANT-BINDING  
PROTEIN, i. mRNA sequence.

|           |            |          |    |            |
|-----------|------------|----------|----|------------|
| ACCESSION | AA977608   | PROTEIN: | ;; | MRNA sequ  |
| VERSION   | AA977608.1 |          |    | GI:3155054 |

|          |              |
|----------|--------------|
| KEYWORDS | EST.         |
| SOURCE   | human.       |
| ORGANISM | Homo sapiens |

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

| REFERENCE<br>AUTHORS<br>TITLE                                                             | JOURNAL<br>COMMENT                                                                        |
|-------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|
| <p>1. <b>W. H. R. WILSON</b><br/> <b>THEORY OF ELASTICITY</b><br/> <b>2ND EDITION</b></p> | <p>1. <b>W. H. R. WILSON</b><br/> <b>THEORY OF ELASTICITY</b><br/> <b>2ND EDITION</b></p> |

1 (bases 1 to 513)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
This clone is available royalty-free through LINL ; contact the  
IMAGE Consortium ([info@image.linn.gov](mailto:info@image.linn.gov)) for further information.  
Insert Length: 727 Std Error: 0.00  
Seq primer: -40m13 fwd. Et from Amersham  
High quality sequence stop: 339.

[illegible]

Query Match 67.2%; Score 465; DB 9; Length 513;  
Best Local Similarity 97.6%; Pred. No. 4.3e-102;  
Matches 493; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

|     |    |                                                                      |     |
|-----|----|----------------------------------------------------------------------|-----|
| 189 | QY | GTGTCCCGCATGAGCTGACAGCCCTTGGCGGTGGGGAGTGTGGAGCCGACGTTCACTTTC         | 248 |
| 513 | Db | GTGTGCCCGAGTGTGACGTGTACAG-CCTTGGCTGTGGAGTGTGGAGCCACGCTTCACTTTC       | 455 |
| 249 | QY | A-TGAGGGAGGATCGGTGATCTCCAGAGAAATCTGATGCGGAGAGACGGAGAGGCGCTGG         | 307 |
| 454 | Db | ACTGAGGGAGGATAGGTGATCTCCAGAGAAATCTGTATGCGGAGAGAGTATGAGAGCGCTGG       | 395 |
| 308 | QY | CAATATACAGCGCTATGCGGGGAGGAGTCACTGATGTAAGTCTGCCACAGAGAGGA             | 367 |
| 394 | Db | CAATATACAGCGCTATGCGGGGAGGAGTCACTGATGTAAGTCTGCCACAGAGAGGA             | 335 |
| 368 | QY | CCACTACTACTCTTTACTTGCAAAGACACGACCATATGAGGGGCGCTGCTCCACATATGAGGAAAGCT | 427 |
| 334 | Db | CCACTACTACTCTTTACTTGCAAAGACACGACCATATGAGGGGCGCTGCTCCACATATGAGGTAAGCT | 275 |
| 428 | QY | TGTGGGTAGGAATTTCTGATTAACACCGGGAGGCGCTTGGAGAGTAATTAAGAAATTTGGTGCA     | 487 |
| 274 | Db | TGTGGGTAGGAATTTCTGATTAACACCGGGAGGCGCTTGGAGAGTAATTAAGAAATTTGGTGCA     | 215 |
| 488 | QY | GGCAGAGGACTCTTCGGAGGAGAGACATATTTACAGGCCCTTGCACAGCGGGAAGCTGCGTTCC     | 547 |
| 214 | Db | GGCAGAGGACTCTTCGGAGGAGAGACATATTTACAGGCCCTTGCACAGCGGGAAGCTGCGTTCC     | 155 |
| 548 | QY | CGAACAATAGGACAGCCCGCGGTCTGCACCTCCAGAGCCCAACCTTACCACACACACACAGA       | 607 |
| 154 | Db | CGAACAATAGGACAGCCCGCGGTCTGCACCTCCAGAGCCCAACCTTACCACACACACACAGA       | 95  |
| 608 | QY | GCCCGGACCACTGTGGACTTACCTTCGACGCATATGACCTTCCCTGCTGCCACCCACTGAC        | 667 |
| 94  | Db | GCTTGACCACTGTGGACTTACCTTCGACGCATATGACCTTCCCTGCTGCCACCCACTGAC         | 35  |
| 668 | QY | TCGAAATTAAGTTCCTTCTCCGCCCA                                           | 692 |
| 34  | Db | TTCAATTAAGTTCCTTCTCCGCCCA                                            | 10  |

RESULT 3  
 A1251747/c  
 LOCUS  
 DEFINITION  
 q10q12.1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:1854287 3' similar to FR:063613 063613 ODORANT-BINDING  
 PROTEIN. ; mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 human.  
 A1251747 477 bp mRNA linear EST 05-NOV-1998  
 IMAGE:1854287 3' similar to FR:063613 063613 ODORANT-BINDING  
 PROTEIN. ; mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 human.  
 A1251747.1 GI:3848276

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 477)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 396.  
 Location/Qualifiers  
 1. 477  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:1854287"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBHL19W, testis NBT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I. M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 79 a 123 c 145 g 130 t

## FEATURES

source  
 1. 477  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:1854287"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBHL19W, testis NBT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I. M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 79 a 123 c 145 g 130 t

BASE COUNT  
 ORIGIN  
 Query Match 66.6%; Score 460.6; DB 9; Length 477;  
 Best Local Similarity 99.1%; Pred. No. 4.9e-101;  
 Matches 463; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 226 AGTTGAGGCGAGCTCAGTTCATGAGGAGGATCGGTGATCCAGCAAGAAATCTGA 285  
 DB 476 AGTTGAGGCGAGCTCAGTTCATGAGGAGGATCGGTGATCCAGCAAGAAATCTGA 417  
 QY 286 TCGGAGAGCGGAGGAGCTCGCAATACAGCGCTATGGGGGCGAGAGCTCATGTACC 345  
 DB 416 TCGGAGAGCGGAGGAGCTCGCAATACAGCGCTATGGGGGCGAGAGCTCATGTACC 357  
 QY 346 TCGAGAGCTGCCAGGAGGAGGAGCTCATCTTTTACATGCAAGAGGAGGAGGAGG 405  
 DB 356 TCGAGAGCTGCCAGGAGGAGGAGCTCATCTTTTACATGCAAGAGGAGGAGGAGG 297  
 QY 406 GCCTGCTCCAGATGGGAGGCTTGTGGTAGGAATCTGATACCAACGGAGGAGGAGG 465  
 DB 296 GCCTGCTCCAGATGGGAGGCTTGTGGTAGGAATCTGATACCAACGGAGGAGGAGG 237  
 QY 466 AGAATTTAGAAATTTGTCAGCGCAAGGAGCTCTGGGAGGAGGAGGAGGAGGAGG 525  
 DB 236 AGAATTTAGAAATTTGTCAGCGCAAGGAGCTCTGGGAGGAGGAGGAGGAGGAGG 177  
 QY 526 TGCAGAGGAGGAGGAGCTGGGTTCCCGAACAACACTAGGAGGAGGAGGAGGAGGAGG 585

DB 176 TCGAGAGCGGAGGAGCTCGTTCGCGAACAACACTAGGAGGAGGAGGAGGAGGAGG 117  
 QY 586 CCACCTTACCACACAGACAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 645  
 DB 116 CCACCTTACCACACAGACAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 57  
 QY 646 TCCCTGCTCCACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 692  
 DB 56 TCCCTGCTCCACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 10

## RESULT 4

A1219510/c  
 LOCUS  
 DEFINITION  
 q12q40.2.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:1845603 3' similar to FR:063613 063613 ODORANT-BINDING  
 PROTEIN. ; mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 human.  
 A1219510 499 bp mRNA linear EST 30-NOV-1998  
 IMAGE:1845603 3' similar to FR:063613 063613 ODORANT-BINDING  
 PROTEIN. ; mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 human.  
 A1219510.1 GI:3801713

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 499)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 330.  
 Location/Qualifiers  
 1. 499  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:1845603"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBHL19W, testis NBT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I. M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 85 a 135 c 151 g 126 t

## FEATURES

source  
 1. 499  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:1845603"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site.1: Not I; Site.2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBHL19W, testis NBT, and B-cell  
 NCI CGAP GCBI) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 I. M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."  
 85 a 135 c 151 g 126 t

BASE COUNT  
 ORIGIN  
 Query Match 65.4%; Score 452.8; DB 9; Length 499;  
 Best Local Similarity 94.2%; Pred. No. 3.8e-99;  
 Matches 469; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 QY 195 CCAGTGGAGTGCAGCGCTCGGCGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 254  
 DB 499 CCAGTGGAGTGCAGCGCTCGGCGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 440  
 QY 255 GAGGATCGGTGCATCAGAGAAATCTGTATGGGAGAGAGGAGGAGGAGGAGGAGGAGG 314  
 DB 439 NAGGATCGGTGCATCAGAGAAATCTGTATGGGAGAGAGGAGGAGGAGGAGGAGG 380  
 QY 315 AGCGCTGTATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374











Query Match 24.5%; Score 169.6; DB 10; Length 626;  
 Best Local Similarity 60.0%; Pred. No. 1.1e-30;  
 Matches 319; Conservative 0; Mismatches 209; Indels 4; Gaps 2;

QY 105 GAGGAGAGATATACAGAGGACCTGTGAGTCAGAGCCATGGTGGCGTCAAGACCTTT 164  
 Db 6 GACCTGGTGGATTTACTCTGGGATCTGGTACGAGAGCCATGGTACATATGATACCTA 65  
 QY 145 CCGGAGGACAGGAGCCAGAGAGGTGTCCTCCAGTGAAGTGAAGCCCTGGGCGGTGG 224  
 Db 66 CCAGTCAACAGATACCCAGTATAGTTTCCCTGTGAGATATAGTCTCGGAGAAGGA 125  
 QY 225 AAGTGGAGCCAGCTTCACTTCATGAGGAGGATCGGTGCATCCAGAGAAGAACTCG 284  
 Db 126 GACTTGGAGACACAGCTGTGATCTGGAAATGCTCATTTGCCGTGAGTTTAAATCGTG 185  
 QY 285 ATGCGGAAGAGGAGGAGCTTGGCAATACAGCGCTATGGGGGAGGAGGCTCATGTAC 344  
 Db 186 ATGAAGAAGACAGAGAGCTTGGCAATACAGCGCTTTCATACAGAGAGGTATTCAT 245  
 QY 345 CTGAGGAGCTGCCAGGAGGAGGACCTACATCTTTTACTGCAAGAGCAGCAGCATGGG 404  
 Db 246 GTGGAAGAGAGCTCGGTGATGAGCAGCTACATTTTCTACTGCGAGGCGGCACAAATGG 305  
 QY 405 GGCGCTG---CTCCACATGGAAGCTGTGGGTAGGATCTCTGATCCACCGGAGGCC 461  
 Db 306 ACCTGCTNTCCGGATGGGAGAGCTCATGGGAGAGAGCTCTGGTGAATCCAGAGGCC 365  
 QY 462 CTGGAAGATTTAGAAATTTGGTGCAGGAGGAGCTCTCGGAGGAGAGCAATTTTCAG 521  
 Db 366 ATGGAGATTTTAAAGATTTTCAATGAAGCGCATGATCTCGGAGTGAAGAGATTTTGG 425  
 QY 522 CCCTGCGAGAGGAGAGCTCGCTTCCGGAACACTAGGAGC-CCCGGGTCTGCACTCC 580  
 Db 426 CAGAGATCGGAGATTAATGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 485  
 QY 581 AGAGCCCACTTACCAACACAGAGAGCCGAGCAGCAGCTGAGACTACCTCC 632  
 Db 486 TGAGCCAGCTTGTCTTCCACACCAAGCTGGGAGATCTCTTCCACACCTC 537

RESULT 11  
 A1877465 519 bp mRNA linear EST 21-JUL-1999  
 LOCUS ud10409.r1 Soares\_NMPu Mus musculus cDNA clone IMAGE:1434737 5'-  
 similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN.; ; mRNA  
 sequence.

ACCESSION A1877465  
 VERSION A1877465.1 GI:5551514  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 519)  
 NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapb-remail.nih.gov](mailto:cgapb-remail.nih.gov)  
 This clone is available royalty-free through LBNL; contact the  
 IMAGE Consortium ([info@image.lbl.gov](mailto:info@image.lbl.gov)) for further information.  
 MGI:918805  
 Putative full length read  
 vector to vector length is  
 Seq primer: 28ml3 rev2 ET from Amersham  
 High quality sequence stop: 503.  
 Location/Qualifiers  
 1. 519  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1434737"

## FEATURES

source

/clone\_lib="Soares\_NMPu"  
 /sex="female"  
 /dev stage="adult"  
 /lab host="DH10s"  
 /notes="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; 1st strand cDNA was prepared from  
 pregnant mouse uterus, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT73  
 vector. Library is normalized. Library was constructed by  
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT 148 a 112 c 142 g 116 t 1 others  
 ORIGIN

Query Match 23.4%; Score 162.2; DB 9; Length 519;  
 Best Local Similarity 59.6%; Pred. No. 6.7e-29;  
 Matches 291; Conservative 0; Mismatches 194; Indels 3; Gaps 1;

QY 39 CTGGAGATGAAGACCTGTTCTCTGGGTGTCAAGCTCTCGGCTGGCGCTGCCCTGCTTC 98  
 Db 27 CTGCTCTCACCATCTCTGCTGCTGGGGCTGGTGGCTGCTCTGAGGCTCAGGAAGCCCG 86  
 QY 99 ACCCTGGAGGAGGAGATATCAGAGGACCTGTGACGTGAGGCGCATGGTGTGATGAG 158  
 Db 87 CCAGATGACCTGGTGGATTTACTCTGGGATCTGGTACCAAGGCCCATGTTACCAATGCT 146  
 QY 159 GACTTTCGGAGAGAGAGGAGGCCAGGAAGGTGTCCTCCAGTGAAGGTGACAGCCCTGGGC 218  
 Db 147 ACCCTACCCAGTCAACAGATACCATGATAGTTTCCCTGTGAGAAATATAGTCTGGAA 206  
 QY 219 GGTGGAGTGTGAAGCCAGCTTCCCTCATGAGGAGGAGATCGGTGCATCCAGAGAAA 278  
 Db 207 GAAGGAGACTTGGAGACCAAGCTGTGATTTCTGGAACAAATGTCATTGCCGTGAGTTAA 266  
 QY 279 ATCTGTATGGGAGAGGAGGAGCTGGCAATACAGAGCGCTATGCGGCGAGGAGCTC 338  
 Db 267 TTCTGTATGAAGAAACAGAGAGGCTGGCAATACAGAGCTTTTCTATACAGAGGTT 326  
 QY 339 ATGTACTGACAGAGCTGCCAGAGGAGGAGCTGATCTTTTACTGCAAGAGAGGAGC 398  
 Db 327 ATTCATGTGAAGAGAGCTCGGTGATGAGGAGCTACATTTCTACTGCGAGAGAGCTCT 386  
 QY 399 CATTGGGGGCTG---CTCCACATGAGGAGAGCTGTGGTGGTAGAATTCGTATACCAACCG 455  
 Db 387 ATGAGGAGCTGCTCATTCGGGATGGGAGAGCTCATGAGGAGAGAGCTCTGGTGAATAATCA 446  
 QY 456 GAGGCGCTGGAAGATTTAAGAAATTTGGTGCAGCGCAAGGAGCTCTCGGAGGAGGAGCA 515  
 Db 447 GAGGCAATGGAAGATTTAAGAAATTTCAAAAGCGCATGAATCTCCGACTGGGAACATG 506  
 QY 516 TTCAGGCC 523  
 Db 507 TTTGTGCC 514

## RESULT 12

R47029

LOCUS

DEFINITION

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029

R47029





BASE COUNT 112 a 109 c 123 g 157 t  
 ORIGIN TAG\_SEQ-CANVG\*  
 Query Match 17.3%; Score 119.8; DB 10; Length 501;  
 Best Local Similarity 60.1%; Pred. No. 1.2e-18;  
 Matches 235; Conservative 0; Mismatches 152; Indels 4; Gaps 2;  
 QY 246 TTCTGAGGAGGATCGGTGATCCAGAGAAATCTGATCGGAGACGGAGAGCCT 305  
 Db 457 TTCTGACATGGTCAATGCGTGAATTTAAATTCGTGATGAGAAACAGAGAGCCT 438  
 QY 306 GGCATATACAGCCCTATGGGGGAGGAGCTCATGTACTGCAGGAGCTGCCAGGAGG 365  
 Db 437 GGCATATACAGCCCTTTTATACACGAGGTTATTCATGTGGAAGAGCTCGGTGAAT 378  
 QY 366 GACCACTACATCTTTTACTGCAAGACACGACCATGGGGGCTG---CTCCACATCGGA 422  
 Db 377 GAGCACTACATTTTCTACTCGAGGGCGGCAATGGGACCTCTCATTCGGGATGGA 318  
 QY 423 AGCTTGTGGTAGGAATTCATACCAACCGGGAGGCCCTGGAGAAATTAAGAAATG 482  
 Db 317 AGCTCATGGGAGAGACTCTGGTGAATCCAGAGGCCCATGGAGAAATTAAGAAATTC 258  
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Search completed: February 10, 2003, 04:58:23  
 Job time : 1928.58 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:02:40 ; Search time 2254.33 Seconds  
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Perfect score: 692

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Scoring table: IDENTITY\_NUC

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Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenBank.\*

2: gb\_hg.\*

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15: em\_ba.\*

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40: em\_hgt\_mus.\*

41: em\_hgtc\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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| 2          | 688.8 | 99.5          | 739    | 6  | AX491098  | Sequence     |
| 3          | 676   | 97.7          | 676    | 6  | AX083544  | Sequence     |
| 4          | 676   | 97.7          | 676    | 6  | AX083544  | Sequence     |
| 5          | 648.8 | 93.8          | 676    | 6  | AX083536  | Sequence     |
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ALIGNMENTS

RESULT 1

AX454620

LOCUS

DEFINITION

Sequence 205 from Patent WO0208284.

AX454620

ACCESSION

AX454620.1

KEYWORDS

human.

SOURCE

ORGANISM

human sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,

Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.

Pred. No. is the number of results predicted by chance to have a

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 205 31-JAN-2002;  
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)  
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Best Local Similarity 99.7%; Pred. No. 7.2e-146;  
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DEFINITION Sequence 205 from Patent WO020690.  
ACCESSION AX491098  
VERSION AX491098.1 GI:22323886  
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SOURCE human.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I., and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 205 03-JAN-2002;  
Genentech, Inc. (US)  
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DEFINITION Sequence 9 from Patent WO0112806.  
ACCESSION AX083544  
VERSION AX083544.1 GI:13185354  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 676)  
AUTHORS Pitiot,G., Lacazette,E. and Gachon,F.  
TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
polypeptides and polynucleotides coding for said polypeptides and  
uses thereof  
JOURNAL Patent: WO 0112806-A 9 22-FEB-2001;  
Universite d'Auvergne (FR); Pitiot, Gilles (FR)  
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gene).  
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VERSION AJ251026.1 GI:6900076  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 676)  
AUTHORS Lacazette,E., Gachon,A.M. and Pitiot,G.  
TITLE A novel human odorant-binding protein gene family resulting from  
genomic duplications at 9q34: differential expression in the oral and  
genital spheres  
JOURNAL Hum. Mol. Genet. 9 (2), 289-301 (2000)  
MEDLINE 20076326  
PUBMED 10607840  
REFERENCE 2 (bases 1 to 676)  
AUTHORS Gachon,A.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM  
U384, Universite d'Auvergne - Faculte de Medecine, 28, place Henri  
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**AUTHORS** Lacazette, E., Gachon, A.M. and Pitiot, G.  
**TITLE** A novel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres  
**JOURNAL** Hum. Mol. Genet. 9 (2), 289-301 (2000)  
**MEDLINE** 20076326  
**PUBLISHED** 10607840

## REFERENCE

**AUTHORS** Gachon, A.M.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (26-OCT-1999) Laboratoire de Biochimie Medicale - INSERM U384, Université d'Auvergne - Faculté de Médecine, 28, place Henri Dunant, Clermont Ferrand cedex 01 63001, FRANCE

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10607840

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 QY 663 CTGACTCCAAATAAAG 678  
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## RESULT 7

AX083538 725 bp DNA linear PAT 28-FEB-2001

LOCUS AX083538 3 from Patent WO0112806.

DEFINITION Sequencing

ACCESSION AX083538

VERSION AX083538.1 GI:13185348

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 725)

AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.

TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof

JOURNAL Patent: WO 0112806-A 3 22-FEB-2001;

Universite d'Auvergne (FR) ; Pitiot, Gilles (FR)

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BASE COUNT 163 a 222 c 217 g 123 t

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Query Match 85.2%; Score 589.8; DB: 6; Length 725;  
 Best Local Similarity 90.9%; Pred. No. 2e-123;  
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 DEFINITION AX083546  
 ACCESSION AX083546  
 VERSION AX083546.1 GI:13185356  
 KEYWORDS human  
 SOURCE human  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 Piliot, G., Jacazette, E. and Gachon, F.  
 Odorant-binding human proteins fixing hydrophobic ligands:  
 polypeptides and polynucleotides coding for said polypeptides and  
 uses thereof  
 Patent: WO 0112806-A 11 22-FEB-2001;  
 Universite d'Auvergne (FR); Piliot, Gilles (FR)  
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Query Match 80.9%; Score 560; DB 6; Length 782;  
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 QY 322 ----- 321  
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 DEFINITION 9008)  
 ACCESSION A251027  
 VERSION A251027.1 GI:6900078  
 KEYWORDS OBPIB gene; odorant binding protein.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.



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ACCESSION AX451327  
VERSION AX451327.1 GI:21698379  
KEYWORDS  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Lok, S., Foster, D.C. and Holloway, J.L.  
TITLE Use of human pheromone polypeptides  
JOURNAL Patent: WO 0223201-A 1 21-MAR-2002;  
ZymoGenetics, Inc. (US)

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Location/Qualifiers

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BASE COUNT 125 a 133 c 172 g 93 t  
ORIGIN

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Best Local Similarity 99.8%; Pred. No. 2.4e-106;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 15  
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LOCUS AX083548  
DEFINITION Sequence 13 from Patent WO0112806.  
ACCESSION AX083548  
VERSION AX083548.1 GI:13185358  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 542)  
AUTHORS Pitiot, G., Lacazette, E. and Gachon, F.  
TITLE Odorant-binding human proteins fixing hydrophobic ligands:  
polypeptides and polynucleotides coding for said polypeptides and  
uses thereof  
JOURNAL Patent: WO 0112806-A 13 22-FEB-2001;  
Universite d'Auvergne (FR); Pitiot, Gilles (FR)

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BASE COUNT 129 a 169 c 155 g 89 t  
ORIGIN

Query Match 61.7%; Score 426.8; DB 6; Length 542;  
Best Local Similarity 99.5%; Pred. No. 1.7e-86;  
Matches 428; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 669 CCAATTAAG 678

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Db 533 CCAATTAAG 542

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Job time : 2261.33 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 19:57:40 ; Search time 254.241 Seconds  
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Sequence: 1 GACGCCAGTGCCTCCGA.....ATTAAGTCCTTCCTCCCA 692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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| 3          | 690         | 99.7  | 690    | AA291770 | Human breast speci  |
| 4          | 688.8       | 99.5  | 738    | AAF54313 | DNA encoding prote  |
| 5          | 688.8       | 99.5  | 739    | AA058615 | Human PRO1283 prot  |
| 6          | 688.8       | 99.5  | 739    | AA037071 | Human PRO1283 (UNQ  |
| 7          | 688.8       | 99.5  | 739    | ABL95663 | Human angiogenesis  |
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| 30 | 145.2 | 21.0 | 525   | 15 | AAH78463 | Human reproductive  |
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PN W09859049-AI.  
XX 30-DEC-1998.  
XX 19-JUN-1998; 98W0-US12862.  
XX 20-JUN-1997; 97US-0879354.  
XX (ABBO) ABBOTT LAB.  
XX Billing-medell PA, Cohen M, Colbitts TL, Friedman PN;  
XX Gordon J, Grandos EN, Hodges SC, Klass MR, Kratochvil JD;  
XX Russell JC, Scheffel CP, Stroupe SD, Fu H;  
XX WPI; 1999-105623/09.  
XX New isolated BS124 polynucleotides and polypeptides - used for

PT detecting, diagnosing, preventing or treating diseases or conditions  
 PT of the breast, such as breast cancer  
 XX Claim 11: Pages 94-95; 125pp; English.

CC The sequence is that of a BSI24-specific EST clone.  
 CC It is useful for detecting, diagnosing, staging, preventing  
 CC or treating, or determining predisposition to diseases or  
 CC conditions of the breast, such as breast cancer.

XX Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;

Query Match 100.0%; Score 692; DB 20; Length 692;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-168;  
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGCCAGTGAAGTGGCGAGTGGCGAGCAGACAGAGCTCTGAGATGAAGACCTGTTC 60  
 Db 1 GAGGCCAGTGAAGTGGCGAGTGGCGAGCAGACAGAGCTCTGAGATGAAGACCTGTTC 60  
 QY 61 TGGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 61 TGGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 QY 121 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 Db 121 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 QY 181 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 Db 181 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 QY 241 TCACTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 Db 241 TCACTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 QY 301 AGCTTGGCAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 Db 301 AGCTTGGCAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 361 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 Db 361 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 QY 421 GAAAGCTTGTGGTAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 Db 421 GAAAGCTTGTGGTAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 QY 481 TGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Db 481 TGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 QY 541 GCGTTCGAGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 Db 541 GCGTTCGAGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 QY 601 ACACAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 Db 601 ACACAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 QY 661 ACCTGATCCCAATTAAGTCTTCTCCGCCCA 692  
 Db 661 ACCTGATCCCAATTAAGTCTTCTCCGCCCA 692

RESULT 2

ID AX07457  
 XX AX07457 standard; cDNA; 692 BP.  
 AC AX07457;  
 XX  
 DT 08-JUN-1999 (first entry)  
 XX

DE Human BSI24 specific EST clone consensus sequence.  
 XX BSI24; breast; cancer; detection; diagnosis; prevention; treatment;  
 KW consensus; EST; ss.  
 XX Homo sapiens.

XX WO9859049-A1.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-US12862.

XX 20-JUN-1997; 97US-0879354.

XX (ABBO ) ABBOTT LAB.

XX Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;

PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;

PI Russell JC, Scheffel CP, Stroupe SD, Yu H;

XX WPI; 1999-105623/09.

XX New isolated BSI24 polynucleotides and polypeptides - used for  
 PT detecting, diagnosing, preventing or treating diseases or conditions  
 PT of the breast, such as breast cancer

XX Claim 11: Page 95; 125pp; English.

XX The sequence is that of a consensus BSI24-specific EST clone.  
 CC It is useful for detecting, diagnosing, staging, preventing  
 CC or treating, or determining predisposition to diseases or  
 CC conditions of the breast, such as breast cancer.

XX Sequence 692 BP; 162 A; 209 C; 205 G; 116 T; 0 other;

Query Match 100.0%; Score 692; DB 20; Length 692;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-168;  
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGCCAGTGAAGTGGCGAGTGGCGAGCAGACAGAGCTCTGAGATGAAGACCTGTTC 60  
 Db 1 GAGGCCAGTGAAGTGGCGAGTGGCGAGCAGACAGAGCTCTGAGATGAAGACCTGTTC 60  
 QY 61 TGGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 Db 61 TGGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 QY 121 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 Db 121 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 QY 181 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 Db 181 CAGGAGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 QY 241 TCACTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 Db 241 TCACTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
 QY 301 AGCTTGGCAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 Db 301 AGCTTGGCAATACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 361 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 Db 361 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 QY 421 GAAAGCTTGTGGTAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 Db 421 GAAAGCTTGTGGTAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 QY 481 TGGTGTGACGCTGCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

[illegible]

|          |                                                                      |
|----------|----------------------------------------------------------------------|
| RESULT 3 |                                                                      |
| AAZ91770 |                                                                      |
| ID       | AAZ91770 standard; DNA; 690 BP.                                      |
| XX       |                                                                      |
| XX       | AAZ91770;                                                            |
| XX       |                                                                      |
| XX       |                                                                      |
| DT       | 01-JUN-2000 (first entry)                                            |
| XX       |                                                                      |
| XX       | Human breast specific gene LS clone 1213903.                         |
| DE       |                                                                      |
| XX       |                                                                      |
| XX       | Human; breast specific gene; breast specific marker; BSG; diagnosis; |
| KW       | breast cancer; therapy; ss.                                          |
| KW       |                                                                      |

|                                  |                                            |                                                                |     |
|----------------------------------|--------------------------------------------|----------------------------------------------------------------|-----|
| Db                               | 51                                         | TGGGTGTCAAGGCTGGCCCTGGCCCGTCCCTGTCTTCACTCCGTGGAGGAGGAGATCA     | 12  |
| QY                               | 121                                        | CAGGGAACCTGGTACGTGAAGGCCATCGTGGTCGATAAAGAGCATTTCCGAGAGACAGAGGC | 180 |
| Db                               | 121                                        | CAGGGAACCTGGTACGTGAAGGCCATCGTGGTCGATAAAGAGCATTTCCGAGAGACAGAGGC | 180 |
| QY                               | 181                                        | CCAGGAAGGTGTGCCCACTGAAGGTGACACAGCCCTGGCGCGTGGGAAGTTGGAAGCCACGT | 240 |
| Db                               | 181                                        | CCAGGAAGGTGTGCCCACTGAAGGTGACACAGCCCTGGCGCGTGGGAAGTTGGAAGCCACGT | 240 |
| QY                               | 241                                        | TCACCTTCATGAGGGAGGATCGGTGTCATCCAGAGAAATCCTGATCGGGAAGACGAGG     | 300 |
| Db                               | 241                                        | TCACCTTCATGAGGGAGGATCGGTGTCATCCAGAGAAATCCTGATCGGGAAGACGAGG     | 300 |
| QY                               | 301                                        | AGCCTGGCAAAATACAGCGCTCATGGCGGCACGAGAGCTCATGTACCTGCAGGAGCTGCCCA | 360 |
| Db                               | 301                                        | AGCCTGGCAAAATACAGCGCTCATGGCGGCACGAGAGCTCATGTACCTGCAGGAGCTGCCCA | 360 |
| QY                               | 361                                        | GGAGGGACACATACATCTTTTACTGCMAAGACACAGACCATGSGGGCCCTGCTCCATGG    | 420 |
| Db                               | 361                                        | GGAGGGACACATACATCTTTTACTGCMAAGACACAGACCATGSGGGCCCTGCTCCATGG    | 420 |
| QY                               | 421                                        | GAAGACCTTGTGGGTAGGAATTCGTATACCAACCGGGAGGCCCTGGAGAAGATTTAAGAAT  | 480 |
| Db                               | 421                                        | GAAGACCTTGTGGGTAGGAATTCGTATACCAACCGGGAGGCCCTGGAGAAGATTTAAGAAT  | 480 |
| QY                               | 481                                        | TGCTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCAACGCCCTGCAGACGCGGAAGCT  | 540 |
| Db                               | 481                                        | TGCTGCAGCGCAAGGGACTCTCGGAGGAGGACATTTTCAACGCCCTGCAGACGCGGAAGCT  | 540 |
| QY                               | 541                                        | GGTGTCCCGAACAATAGCAGAGCCCGGGCTGCACTTCGAGAGCCCACTTCACACAG       | 600 |
| Db                               | 541                                        | GGTGTCCCGAACAATAGCAGAGCCCGGGCTGCACTTCGAGAGCCCACTTCACACAG       | 600 |
| QY                               | 601                                        | ACACAGAGCCCGGACCACTTGGACCTACCTCCACGACATFACACCTTCCTGCTCCACCC    | 660 |
| Db                               | 601                                        | ACACAGAGCCCGGACCACTTGGACCTACCTCCACGACATFACACCTTCCTGCTCCACCC    | 660 |
| QY                               | 661                                        | ACCTGACTCCCAATAAAGTCCTTCTCCGCC                                 | 690 |
| Db                               | 661                                        | ACCTGACTCCCAATAAAGTCCTTCTCCGCC                                 | 690 |
| RESULT 4                         |                                            |                                                                |     |
| AAAF54313 standard; DNA; 738 bp. |                                            |                                                                |     |
| XX                               | AC                                         | AAAF54313;                                                     |     |
| XX                               | AC                                         |                                                                |     |
| DT                               | 02-APR-2001 (first entry)                  |                                                                |     |
| XX                               |                                            |                                                                |     |
| DE                               | DNA encoding protein of the invention #50. |                                                                |     |
| XX                               |                                            |                                                                |     |
| XX                               | Secreted; transmembrane; gene therapy; ss. |                                                                |     |
| KW                               |                                            |                                                                |     |

|          |                                            |
|----------|--------------------------------------------|
| RESULT 4 |                                            |
| AAAF5313 |                                            |
| ID       | AAF5313 standard; DNA; 738 BP.             |
| XX       |                                            |
| XX       | AAF5313;                                   |
| XX       |                                            |
| XX       | 02-APR-2001 (first entry)                  |
| XX       |                                            |
| XX       | DNA encoding protein of the invention #50. |
| XX       |                                            |
| XX       | Secreted; transmembrane; gene therapy; ss. |
| XX       |                                            |
| XX       | Unidentified.                              |
| XX       |                                            |
| XX       | WO200078961-A1.                            |
| PN       |                                            |
| XX       |                                            |
| XX       | 28-DEC-2000.                               |
| PD       |                                            |
| XX       |                                            |
| XX       | 18-FEB-2000; 2000WO-US04342.               |
| XX       |                                            |
| PR       | 23-JUN-1999; 99US-0141037.                 |
| PR       | 20-JUL-1999; 99US-0144758.                 |
| PR       | 26-JUL-1999; 99US-0145698.                 |
| PR       | 01-SEP-1999; 99WO-US20111.                 |
| PR       | 29-OCT-1999; 99US-0162506.                 |
| PR       | 30-NOV-1999; 99WO-US28313.                 |
| PR       | 02-DEC-1999; 99WO-US28551.                 |
| PR       | 16-DEC-1999; 99WO-US30095.                 |
| PR       | 05-JAN-2000; 2000WO-US00219.               |
| PR       | 06-JAN-2000; 2000WO-US00376.               |



PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX (GENTH) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V,  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WL, Yan M;  
 XX P-PSDB; AAB33450.  
 DR WPI: 2000-572271/53.  
 DR P-PSDB; AAB33450.  
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PI immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 23; Fig 73; 309pp; English.  
 XX The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC and peripheral nervous systems, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;

Query Match 99.5%; Score 688.8; DB 21; Length 739;  
 Best Local Similarity 99.7%; Pred. NO. 2.9e-167;  
 Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GACGCCAGTGTACCTGCGAGTGGCAGCAGAGCTCTGGAGATGAAGACCTGTTC 60  
 DB 1 GACGCCAGTGTACCTGCGAGTGGCAGCAGAGCTCTGGAGATGAAGACCTGTTC 60  
 QY 61 TGGGTGTACGCTGCGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 DB 61 TGGGTGTACGCTGCGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
 QY 121 CAGGAGCTGTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 DB 121 CAGGAGCTGTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 QY 181 CAGGAGGAGTGTCCCATGTAAGGTGACAGCCCTGGGCGGTGGGAAGTGGAGCCACGT 240  
 DB 181 CAGGAGGAGTGTCCCATGTAAGGTGACAGCCCTGGGCGGTGGGAAGTGGAGCCACGT 240  
 QY 241 TCACCTTATGAGGAGGAGTGGTGCATCCAGAGAAATCTCTGATCGGAGAGCAGGAG 300  
 DB 241 TCACCTTATGAGGAGGAGTGGTGCATCCAGAGAAATCTCTGATCGGAGAGCAGGAG 300  
 QY 301 AGCTTGGCAATATACAGCGCTATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 DB 301 AGCTTGGCAATATACAGCGCTATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
 QY 361 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

DB 361 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420  
 QY 421 GAAAGCTTGTGGTAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 DB 421 GAAAGCTTGTGGTAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 QY 481 TGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 DB 481 TGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540  
 QY 541 GGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 DB 541 GGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 QY 601 ACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 DB 601 ACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
 QY 661 ACCTGACTCCAAATAAGTCTCTCCGCCCA 692  
 DB 661 ACCTGACTCCAAATAAGTCTCTCTCCGCCCA 692  
 RESULT 6  
 AAA37071  
 ID AAA37071 standard; cDNA; 739 BP.  
 AC AAA37071;  
 XX 08-AUG-2000 (first entry)  
 DE Human PRO1283 (UNQ553) cDNA sequence SEQ ID NO:161.  
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;  
 KW ss.  
 OS Homo sapiens.  
 XX  
 XX WO200012708-A2.  
 XX 09-MAR-2000.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 01-SEP-1998; 98US-0098716.  
 PR 01-SEP-1998; 98US-0098719.  
 PR 01-SEP-1998; 98US-0098750.  
 PR 02-SEP-1998; 98US-0098803.  
 PR 02-SEP-1998; 98US-0098821.  
 PR 02-SEP-1998; 98US-0098843.  
 PR 02-SEP-1998; 98US-0098936.  
 PR 02-SEP-1998; 98US-0098956.  
 PR 02-SEP-1998; 98US-0098962.  
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 PR 02-SEP-1998; 98US-0098973.  
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 PR 02-SEP-1998; 98US-0098979.  
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 PR 02-SEP-1998; 98US-0099002.  
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 PR 02-SEP-1998; 98US-0099123.  
 PR 02-SEP-1998; 98US-0099124.  
 PR 02-SEP-1998; 98US-0099125.  
 PR 02-SEP-1998; 98US-0099126.  
 PR 02-SEP-1998; 98US-0099127.  
 PR 02-SEP-1998; 98US-0099128.  
 PR 02-SEP-1998; 98US-0099129.  
 PR 02-SEP-1998; 98US-0099130.  
 PR 02-SEP-1998; 98US-0099131.  
 PR 02-SEP-1998; 98US-0099132.  
 PR 02-SEP-1998; 98US-0099133.  
 PR 02-SEP-1998; 98US-0099134.  
 PR 02-SEP-1998; 98US-0099135.  
 PR 02-SEP-1998; 98US-0099136.  
 PR 02-SEP-1998; 98US-0099137.  
 PR 02-SEP-1998; 98US-0099138.  
 PR 02-SEP-1998; 98US-0099139.  
 PR 02-SEP-1998; 98US-0099140.  
 PR 02-SEP-1998; 98US-0099141.  
 PR 02-SEP-1998; 98US-0099142.  
 PR 02-SEP-1998; 98US-0099143.  
 PR 02-SEP-1998; 98US-0099144.  
 PR 02-SEP-1998; 98US-0099145.  
 PR 02-SEP-1998; 98US-0099146.  
 PR 02-SEP-1998; 98US-0099147.  
 PR 02-SEP-1998; 98US-0099148.  
 PR 02-SEP-1998; 98US-0099149.  
 PR 02-SEP-1998; 98US-0099150.  
 PR 02-SEP-1998; 98US-0099151.  
 PR 02-SEP-1998; 98US-0099152.  
 PR 02-SEP-1998; 98US-0099153.  
 PR 02-SEP-1998; 98US-0099154.  
 PR 02-SEP-1998; 98US-0099155.  
 PR 02-SEP-1998; 98US-0099156.  
 PR 02-SEP-1998; 98US-0099157.  
 PR 02-SEP-1998; 98US-0099158.  
 PR 02-SEP-1998; 98US-0099159.  
 PR 02-SEP-1998; 98US-0099160.  
 PR 02-SEP-1998; 98US-0099161.  
 PR 02-SEP-1998; 98US-0099162.  
 PR 02-SEP-1998; 98US-0099163.  
 PR 02-SEP-1998; 98US-0099164.  
 PR 02-SEP-1998; 98US-0099165.  
 PR 02-SEP-1998; 98US-0099166.  
 PR 02-SEP-1998; 98US-0099167.  
 PR 02-SEP-1998; 98US-0099168.  
 PR 02-SEP-1998; 98US-0099169.  
 PR 02-SEP-1998; 98US-0099170.  
 PR 02-SEP-1998; 98US-0099171.  
 PR 02-SEP-1998; 98US-0099172.  
 PR 02-SEP-1998; 98US-0099173.  
 PR 02-SEP-1998; 98US-0099174.  
 PR 02-SEP-1998; 98US-0099175.  
 PR 02-SEP-1998; 98US-0099176.  
 PR 02-SEP-1998; 98US-0099177.  
 PR 02-SEP-1998; 98US-0099178.  
 PR 02-SEP-1998; 98US-0099179.  
 PR 02-SEP-1998; 98US-0099180.  
 PR 02-SEP-1998; 98US-0099181.  
 PR 02-SEP-1998; 98US-0099182.  
 PR 02-SEP-1998; 98US-0099183.  
 PR 02-SEP-1998; 98US-0099184.  
 PR 02-SEP-1998; 98US-0099185.  
 PR 02-SEP-1998; 98US-0099186.  
 PR 02-SEP-1998; 98US-0099187.  
 PR 02-SEP-1998; 98US-0099188.  
 PR 02-SEP-1998; 98US-0099189.  
 PR 02-SEP-1998; 98US-0099190.  
 PR 02-SEP-1998; 98US-0099191.  
 PR 02-SEP-1998; 98US-0099192.  
 PR 02-SEP-1998; 98US-0099193.  
 PR 02-SEP-1998; 98US-0099194.  
 PR 02-SEP-1998; 98US-0099195.  
 PR 02-SEP-1998; 98US-0099196.  
 PR 02-SEP-1998; 98US-0099197.  
 PR 02-SEP-1998; 98US-0099198.  
 PR 02-SEP-1998; 98US-0099199.  
 PR 02-SEP-1998; 98US-0099200.



Db 301 AGCTGCGCAATACAGCGCCTATGGGGGAGGAGCTCATGTACTGAGGAGCTGCCCA 360  
QY 361 GGAGGACCACTACATCTTTTACTGCAAGACCAAGACCACTATGGGGGCTGCTCCACATGG 420  
Db 361 GGAGGACCACTACATCTTTTACTGCAAGACCAAGACCACTATGGGGGCTGCTCCACATGG 420  
QY 421 GAAAGCTTGTGGTAGAATTTGATACCAACCGGAGGAGGCTGGAAGAATTTAGAAAT 480  
Db 421 GAAAGCTTGTGGTAGAATTTGATACCAACCGGAGGAGGCTGGAAGAATTTAGAAAT 480  
QY 481 TGGTGCAGCGAAGGAGCTCTGGAGGAGGAGCATTTTCACGGCCCTCGAGAGGAGCT 540  
Db 481 TGGTGCAGCGAAGGAGCTCTGGAGGAGGAGCATTTTCACGGCCCTCGAGAGGAGCT 540  
QY 541 GCGTTCCGCAACTAGGAGCGCCCGGGTCTGACCTCCAGAGCGCCACCTTACACAG 600  
Db 541 GCGTTCCGCAACTAGGAGCGCCCGGGTCTGACCTCCAGAGCGCCACCTTACACAG 600  
QY 601 ACACAGAGCGGACCACTGAGGAGCTACCTCCAGGAGGAGGAGCTTCCCTGCTCCACAC 660  
Db 601 ACACAGAGCGGACCACTGAGGAGCTACCTCCAGGAGGAGGAGCTTCCCTGCTCCACAC 660  
QY 661 AACTGACTCCAAATAAAGTCTCTCCGCCCA 692  
Db 661 AACTGACTCCAAATAAAGTCTCTCCGCCCA 692

RESULT 7  
ABL95663  
ID ABL95663 standard; cdna; 739 BP.  
AC ABL95663;  
XX  
DT 19-JUL-2002 (first entry)  
XX  
DE Human angiogenesis related cDNA PRO1283 SEQ ID NO: 205.  
XX  
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiast; cytostatic; antiangiogenic; hypotensive; vulnerary;  
KW antiarteriosclerotic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200208284-A2.  
XX  
PD 31-JAN-2002.  
XX  
PF 09-JUL-2001; 2001WO-US21735.  
XX  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US209710.  
PR 02-AUG-2000; 2000US-222895P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23528.  
PR 07-SEP-2000; 2000US-230978P.  
PR 15-SEP-2000; 2000US-000000P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 10-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US30873.  
PR 20-DEC-2000; 2000US-074259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.

PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 28-JUN-2001; 2001WO-US00000.  
XX (GETH) GENENTECH INC.  
PA (BAKE) BAKER K P.  
PA (FERA) FERRARA N.  
PA (GERB) GERBER H.  
PA (GERG) GERRITSEN M E.  
PA (GODD) GODDARD A.  
PA (GODO) GODOWSKI P J.  
PA (GURN) GURNEY A L.  
PA (HILL) HILLAN K J.  
PA (MARS) MARSTERS S A.  
PA (PANJ) PAN J.  
PA (PAON) PAONI N F.  
PA (STEP) STEPHAN J F.  
PA (WATA) WATANABE C K.  
PA (WILL) WILLIAMS P M.  
PA (WOOD) WOOD W I.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Paoni NF;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
DR WPI: 2002-171999/22.  
XX  
DR P-PSDB: ABB95525.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX  
PS Claim 1: Fig 205; 567pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.  
XX  
SQ Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;  
Query Match 99.5%; Score 688.8; DB 24; Length 739;  
Best Local Similarity 99.7%; Pred. No. 2.9e-167;  
Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAGCGCCAGTGTGACTTGGCCGAGGTGGCAGCAGAGCTCTGGAGATGAAGACCTGTTC 60  
Db 1 GAGCGCCAGTGTGACTTGGCCGAGGTGGCAGCAGAGCTCTGGAGATGAAGACCTGTTC 60  
QY 61 TGGGTGTGACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 120  
Db 61 TGGGTGTGACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 120  
QY 121 CAGGAGCTGTGATCTGAGGCGCCATGCTGTGCTGATAGGACTTTCCGGAGCAGAGGAG 180  
Db 121 CAGGAGCTGTGATCTGAGGCGCCATGCTGTGCTGATAGGACTTTCCGGAGCAGAGGAG 180  
QY 181 CCAGGAAGTGTGTCCCGCAGTGAAGGTGACACCCCTGGCGGTGGGAAGTGTGAAGCCAC 240

Db 181 CAGGAAGGTGTCCCACTGAAGTGCACAGCTCTGGCGGTGGGAAGTTGGAAGCCAGT 240  
QY 241 TCACCTTCATGAGGAGGATGCTGTGTCATCAGAGAAAATCTGTATCGAAGACGAGG 300  
Db 241 TCACCTTCATGAGGAGGATGCTGTGTCATCAGAGAAAATCTGTATCGAAGACGAGG 300  
QY 301 AGCTTGGCAATACAGCGCTATGGGCGCAGAGCACTGATGACCTGAGGAGTGCCTA 360  
Db 301 AGCTTGGCAATACAGCGCTATGGGCGCAGAGCACTGATGACCTGAGGAGTGCCTA 360  
QY 361 GGAGGAGCACTACATCTTTTACTGCAAGACGACCAATGGGGGCTGCTCCACATGG 420  
Db 361 GGAGGAGCACTACATCTTTTACTGCAAGACGACCAATGGGGGCTGCTCCACATGG 420  
QY 421 GAAAGCTTGTGGTAGGAATCTGTATACCAACGGGAGGCGCTTGAAGAATTTAAGAAAT 480  
Db 421 GAAAGCTTGTGGTAGGAATCTGTATACCAACGGGAGGCGCTTGAAGAATTTAAGAAAT 480  
QY 481 TGGTGCAGCGCAAGGAGTCTCGAGGAGGACATTTTCAAGCGCCCTCGACAGCGAAGCT 540  
Db 481 TGGTGCAGCGCAAGGAGTCTCGAGGAGGACATTTTCAAGCGCCCTCGACAGCGAAGCT 540  
QY 541 GCCTTCCGCAACACTAGCAGCGCCCGGCTGTCACCTCCAGAGCCACCCCTACCCAG 600  
Db 541 GCCTTCCGCAACACTAGCAGCGCCCGGCTGTCACCTCCAGAGCCACCCCTACCCAG 600  
QY 601 ACACAGAGCCGCGACCTGAGCTACCTGACCGACCTGACCGACCTGCTGCTGCTGACCC 660  
Db 601 ACACAGAGCCGCGACCTGAGCTACCTGACCGACCTGACCGACCTGCTGCTGCTGACCC 660  
QY 661 ACCTGACTCCAAATTAAGTCTCTCCGCCCA 692  
Db 661 ACCTGACTCCAAATTAAGTCTCTCTCCGCCCA 692

RESULT 8  
ABL88174  
ID ABL88174 standard; cDNA; 739 BP.  
XX AC ABL88174;  
XX DT 16-MAY-2002 (first entry)  
XX DE Human PRO1283 cDNA sequence SEQ ID NO:205.  
XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
XX KW gene therapy; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX KW angiogenic disorder; cardiovascular disorder; endothelial disorder; cancer;  
XX KW age-related macular degeneration; cardiac hypertrophy; atherosclerosis; hypertension;  
XX KW rheumatoid arthritis; myocardial infarction; arterial restenosis; angina;  
XX KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX KW wound healing; chromosome mapping; gene mapping; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200200690-A2.  
XX PD 03-JAN-2002.  
XX PF 20-JUN-2001; 2001WO-US19692.  
XX PR 23-JUN-2000; 2000US-213637P.  
XX PR 20-JUL-2000; 2000US-219556P.  
XX PR 25-JUL-2000; 2000US-220624P.  
XX PR 28-JUL-2000; 2000US-220664P.  
XX PR 02-AUG-2000; 2000WO-US20710.  
XX PR 17-AUG-2000; 2000US-222695P.  
XX PR 23-AUG-2000; 2000WO-US23522.  
XX PR 24-AUG-2000; 2000WO-US23328.  
XX PR 07-SEP-2000; 2000US-230978P.

PR 18-SEP-2000; 2000US-0664610.  
PR 18-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-070923B.  
PR 10-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2000US-076609.  
PR 28-FEB-2001; 2000US-076609.  
PR 01-MAR-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-0806666.  
PR 14-MAR-2001; 2001US-0806689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
XX (GETH ) GENENTECH INC.  
XX PA Baker RP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NF;  
XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Ye W;  
XX PI Stephan JF, Metanabe CK, Williams PM, Wood WI, Ye W;  
XX DR WPI; 2002-090516/12.  
XX DR P-PSDB; ABB84919.  
XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX PT infarction), endothelial or angiogenic disorders in a mammal -  
XX PS Claim 2; Fig 205; 565pp; English.  
XX CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
XX CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
XX CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
XX CC activities, and can be used in gene therapy. The PRO polynucleotides,  
XX CC proteins, agonists and antagonists are useful for treating or diagnosing  
XX CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
XX CC e.g. cardiac hypertrophy, trauma, cancer, age-related restenosis,  
XX CC degeneration, atherosclerosis, hypertension, arterial infarction, thrombophlebitis,  
XX CC rheumatoid arthritis, angina, myocardial infarction, breast carcinoma, liver  
XX CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
XX CC carcinoma) and wound healing. The PRO polynucleotides have applications  
XX CC in molecular biology, including use as hybridisation probes, and in  
XX CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
XX CC probes used in the exemplification of the present invention.  
XX SQ Sequence 739 BP; 210 A; 207 C; 205 G; 117 T; 0 other;  
Query Match 99.5%; Score 688.8; DB 24; Length 739;  
Best Local Similarity 99.7%; Pred. No. 2.9e-167;  
Matches 690; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GACGCCCACTGACTGCGGAGTGGGCGCAGCAGAGCTCTGAGATGAGAGCCCTGTCC 60  
Db 1 GACGCCCACTGACTGCGGAGTGGGCGCAGCAGAGCTCTGAGATGAGAGCCCTGTCC 60  
QY 61 TGGGTGTACAGCTCGGCTTGGCGCTGCGCTTGTCTTTCACCTCGAGAGGAGATATCA 120  
Db 61 TGGGTGTACAGCTCGGCTTGGCGCTGCGCTTGTCTTTCACCTCGAGAGGAGATATCA 120  
QY 121 CAGGAGCACTGTGTACGTGAAGGCCATGTGTGTGATAGGACTTTCCCGGAGGACAGGAGC 180  
Db 121 CAGGAGCACTGTGTACGTGAAGGCCATGTGTGTGATAGGACTTTCCCGGAGGACAGGAGC 180



QY 181 CCAGAGAGTGTCCACCTGAAGGTGACAGCCCTGGGGGTGGGAAGTTGGAAGCCACT 240  
 DB 181 CCAGAGAGTGTCCACCTGAAGGTGACAGCCCTGGGGGTGGGAAGTTGGAAGCCACT 240  
 QY 241 TCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCTGATGCGAGAGCGAGG 300  
 DB 241 TCACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCTGATGCGAGAGCGAGG 300  
 QY 301 AGCTTGGCAATACAGCGCTATGCGGGGCGAGAGCTCATGTACTCGAGAGCTGCCA 360  
 DB 301 AGCTTGGCAATACAGCGCTATGCGGGGCGAGAGCTCATGTACTCGAGAGCTGCCA 360  
 QY 361 GGAGGGACCACTACATCTTTTACTGCAAGAGCAGACCATGGGGGCTGTCTCCATGG 420  
 DB 361 GGAGGGACCACTACATCTTTTACTGCAAGAGCAGACCATGGGGGCTGTCTCCATGG 420  
 QY 421 GAAAGCTTGTGGTAGGAATCTGATACCAACCGGAGGCGCTTGAAGAATTTAAGAA 480  
 DB 421 GAAAGCTTGTGGTAGGAATCTGATACCAACCGGAGGCGCTTGAAGAATTTAAGAA 480  
 QY 481 TGGTTCAGCGCAAGGAGCTCTCGAGGAGGACATTTTCAAGCGCTCGAGAGCGGAAGCT 540  
 DB 481 TGGTTCAGCGCAAGGAGCTCTCGAGGAGGACATTTTCAAGCGCTCGAGAGCGGAAGCT 540  
 QY 541 GGGTTCCGACACTAGGAGCGCGGGGTCTGCACTCCAGAGCGCCCTTACCACAG 600  
 DB 541 GGGTTCCGACACTAGGAGCGCGGGGTCTGCACTCCAGAGCGCCCTTACCACAG 600  
 QY 601 ACAGAGCGCGGACGCTGAGCTTACCTCCAGCGGAGCGCTTACCTCCAGCGCGG 660  
 DB 601 ACAGAGCGCGGACGCTGAGCTTACCTCCAGCGGAGCGCTTACCTCCAGCGCGG 660  
 QY 661 ACCTGACTCAAAATAGTCTTTTCCCGCA 692  
 DB 661 ACCTGACTCAAAATAGTCTTTTCCCGCA 692

RESULT 9  
 AAF80043  
 ID AAF80043 standard; cDNA; 676 BP.  
 AC AAF80043;  
 XX 11-JUN-2001 (first entry)  
 DE Nucleotide sequence of odorant binding polypeptide OBPIB-alpha.  
 KW Odorant binding polypeptide; OBPIB; hydrophobic ligand; odorant; allergy;  
 KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;  
 KW anticancer; foetus detoxification; pregnancy marker; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 43..555  
 FT /\*tag= a  
 FT /product= "odorant binding polypeptide OBPIB-alpha"  
 XX WO200112806-A2.  
 PN 22-FEB-2001.  
 XX 11-AUG-2000; 2000WO-FR02319.  
 XX 12-AUG-1999; 99FR-0010439.  
 PR (GVAU-) UNIV AUVERGNE.  
 PA (PITI/) PITOT G.  
 XX Pitiot G, Lacazette E, Gachon F;  
 XX WPI; 2001-202864/20.

DR P-PSDB; AAB67742.  
 XX New human odorant-binding proteins, useful for solubilising lipophilic  
 PT compounds in the transportation of anticancer agents or for slow  
 PT release of perfumes  
 XX Disclosure; Page 113-114; 132pp; French.  
 XX The present sequence encodes a human odorant binding polypeptide (OBP),  
 CC designated OBPIB-alpha. OBPs provide long-term retention (gradual  
 CC release) of lipophilic compounds, so prolong the 'hold' of perfumes,  
 CC deodorants etc. OBP polypeptides are used as binding proteins for  
 CC hydrophobic ligands (particularly odorants); as competitive inhibitors  
 CC (agonists or antagonists) of cellular lipocalin receptors; to detect  
 CC specific antibodies for diagnosis of allergy, asthma or cancer; for  
 CC controlling volatilisation of an odorant, specifically in perfumes;  
 CC cosmetics or disinfectant compositions; to screen compounds, especially  
 CC odorants or flavours, e.g. human pheromones, for binding to OBP, also in  
 CC analysis of complex perfume mixtures; to solubilise lipophilic compounds;  
 CC for treating hyperlipidemia or obesity, or to supplement non-material  
 CC milk when combined with nutritional fatty acids, as food additives; as a  
 CC transporter of pharmaceuticals, especially anticancer agents (providing  
 CC delayed release) but also for delivery across the placental barrier  
 CC (e.g. for detoxification of the foetus); as a marker of pregnancy or  
 CC foeto-placental pathology (rupture of the amniotic membrane); and as  
 CC anti-allergic agents.  
 XX Sequence 676 BP; 160 A; 200 C; 204 G; 112 T; 0 other;  
 SQ  
 Query Match 97.7%; Score 676; DB 22; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-164;  
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 CCCCCAGTACCTCGGAGTGGCGAGCAGACGCTCTGGAGATGAGACCCCTTCTCTG 62  
 DB 1 CCCCCAGTACCTCGGAGTGGCGAGCAGACGCTCTGGAGATGAGACCCCTTCTCTG 60  
 QY 63 GGTGTACGCTCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122  
 DB 61 GGTGTACGCTCGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 QY 123 GGGACCTGTGTACGTGAAGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 182  
 DB 121 GGGACCTGTGTACGTGAAGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 QY 183 AGGAGGTGTCCCGAGTGAAGGTGACAGCCCTGGGGGTGGGAAGTTGGAAGCCAGCTTC 242  
 DB 181 AGGAGGTGTCCCGAGTGAAGGTGACAGCCCTGGGGGTGGGAAGTTGGAAGCCAGCTTC 240  
 QY 243 ACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCTTGAAGCGGAGAGGAGAG 302  
 DB 241 ACCTTCATGAGGAGGATCGTGCATCCAGAGAAATCTTGAAGCGGAGAGGAGAG 300  
 QY 303 CTTGGCAATACAGCGCTATGCGGGGCGAGAGCTCATGTACTCGAGAGCTGCTCCAGG 362  
 DB 301 CTTGGCAATACAGCGCTATGCGGGGCGAGAGCTCATGTACTCGAGAGCTGCTCCAGG 360  
 QY 363 AGGACCACTACATCTTTTACTGCAAGAGCAGACCATGGGGGCTGTCTCCATGGGA 422  
 DB 361 AGGACCACTACATCTTTTACTGCAAGAGCAGACCATGGGGGCTGTCTCCATGGGA 420  
 QY 423 AAGCTTGTGGTAGGAATCTGATACCAACCGGAGGCGCTTGAAGAATTTAAGAATTTG 482  
 DB 421 AAGCTTGTGGTAGGAATCTGATACCAACCGGAGGCGCTTGAAGAATTTAAGAATTTG 480  
 QY 483 GTGAGCGAGAGGAGCTCTCGAGGAGGACATTTTCAAGCGCTCGAGAGCGGAGCTGC 542  
 DB 481 GTGAGCGAGAGGAGCTCTCGAGGAGGACATTTTCAAGCGCTCGAGAGCGGAGCTGC 540  
 QY 543 GTTCCGAGACTAGGAGCGCGGGGTCTGCACTCGAGAGCGCCCTTACCACAGAG 602  
 DB 541 GTTCCGAGACTAGGAGCGCGGGGTCTGCACTCGAGAGCGCCCTTACCACAGAG 600



XX PN WO200112806-A2.  
 XX PD 22-FEB-2001.  
 XX PF 11-AUG-2000; 2000WO-FR02319.  
 XX PR 12-AUG-1999; 99FR-0010439.  
 XX PA (UYAU-) UNIV AUVERGNE.  
 XX PA (PITI/) PITIOT G.  
 XX PI Pitiot G, Lacazette E, Gachon F;  
 XX DR WPI: 2001-202864/20.  
 XX DR P-PSDB; AAB67739.  
 XX PT New human odorant-binding proteins, useful for solubilising lipophilic  
 XX PT compounds in the transportation of anticancer agents or for slow  
 XX PT release of perfumes  
 XX PS Claim 6; Page 108-109; 132pp; French.  
 XX CC The present sequence encodes a human odorant binding polypeptide (OBP),  
 CC designated OBPIA-beta. OBPs provide long-term retention (gradual  
 CC release) of lipophilic compounds, so prolong the 'hold' of perfumes,  
 CC deodorants etc.. OBP polypeptides are used as binding proteins for  
 CC hydrophobic ligands (particularly odorants); as competitive inhibitors  
 CC (agonists or antagonists) of cellular lipocalin receptors; to detect  
 CC specific antibodies for diagnosis of allergy, asthma or cancer; for  
 CC controlling volatilisation of an odorant, specifically in perfumes;  
 CC cosmetics or disinfectant compositions; to screen compounds, especially  
 CC odorants or flavours, e.g. human pheromones for binding to OBP also in  
 CC analysis of complex perfume mixtures; to solubilise lipophilic compounds;  
 CC for treating hyperlipidemia or obesity, or to supplement non-maternal  
 CC milk when combined with nutritional fatty acids, as food additives; as a  
 CC transporter of pharmaceuticals, especially anticancer agents (providing  
 CC delayed release) but also for delivery across the placental barrier  
 CC (e.g. for detoxification of the foetus); as a marker of pregnancy or  
 CC foeto-placental pathology (rupture of the amniotic membrane); and as  
 CC antiallergic agents.  
 XX SQ Sequence 725 BP; 163 A; 222 C; 217 G; 123 T; 0 other;  
 Query Match 85.2%; Score 589.8; DB 22; Length 725;  
 Best Local Similarity 90.9%; Pred. No. 7.7e-142;  
 Matches 659; Conservative 0; Mismatches 17; Indels 49; Gaps 1;  
 QY 3 CGCCGAGTGAAGTCCGAGTGGCGACGACGACGCTCTGGAGTGAAGACCTCTGCTG 62  
 DB 1 CGCCGAGTGAAGTCCGAGTGGCGACGACGACGCTCTGGAGTGAAGACCTCTGCTG 60  
 QY 63 GGTGTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 122  
 DB 61 GGTGTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 120  
 QY 123 GGGACCTGGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182  
 DB 121 GGGACCTGGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 QY 183 AGGAAGTGTCCCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 242  
 DB 181 AGGAAGTGTCCCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 240  
 QY 243 ACCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 302  
 DB 241 ACCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
 QY 303 CTGTGCAATACAGCGCTATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 362  
 DB 301 CTGTGCAATACAGCGCTATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 363 AGGGACCACTACATCTTTTACTGCAAGACCAAGACCACTGCGGGGCTGCTCCACACCTG 422

DB 361 ACGGACGACTAGTCTTTTACTGCAAGACCAAGACCACTGCGGGGCTGCTCCACACCTG 420  
 QY 423 AAGCTGTG-----GG 433  
 DB 421 AAGCTGTGCGGGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 480  
 QY 434 TAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493  
 DB 481 TAGGAATTTCTGATACCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 QY 494 GGGACTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 553  
 DB 541 GGGACTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
 QY 554 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613  
 DB 601 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 QY 614 ACCACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673  
 DB 661 ACCACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 QY 674 TAAG 678  
 DB 721 TAAG 725

RESULT 12  
 AAF80041  
 ID AAF80041 standard; cDNA; 741 BP.  
 AC AAF80041;  
 XX AAF80041;  
 DT 11-JUN-2001 (first entry)  
 XX Nucleotide sequence of odorant binding polypeptide OBPIA-gamma.  
 DE Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy;  
 KW asthma; cancer; perfume; hyperlipidemia; obesity; food additive;  
 KW anticancer; foetus detoxification; pregnancy marker; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FT 43..729  
 FT CDS /\*tag= a  
 FT /product= "odorant binding polypeptide OBPIA-gamma"  
 XX WO200112806-A2.  
 XX PD 22-FEB-2001.  
 XX 11-AUG-2000; 2000WO-FR02319.  
 XX 12-AUG-1999; 99FR-0010439.  
 XX (UYAU-) UNIV AUVERGNE.  
 XX (PITI/) PITIOT G.  
 XX Pitiot G, Lacazette E, Gachon F;  
 XX DR WPI: 2001-202864/20.  
 XX DR P-PSDB; AAB67740.  
 XX New human odorant-binding proteins, useful for solubilising lipophilic  
 XX compounds in the transportation of anticancer agents or for slow  
 XX release of perfumes  
 XX PS Claim 6; Page 109-110; 132pp; French.  
 XX CC The present sequence encodes a human odorant binding polypeptide (OBP),  
 CC designated OBPIA-gamma. OBPs provide long-term retention (gradual







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 20:30:25 ; Search time 50.2996 Seconds  
(without alignments)  
4219.129 Million cell updates/sec

Title: US-09-099-823-5  
Perfect score: 692  
Sequence: 1 GAGCCCCAGTACCTGCGGA.....ATAAAGTCTTCTTCCCCCA 692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY

| Result No. | Score | Query Match | Length | DB | ID               | Description       |
|------------|-------|-------------|--------|----|------------------|-------------------|
| 1          | 514.4 | 74.3        | 522    | 3  | US-09-130-663-1  | Sequence 1, Appl  |
| 2          | 514.4 | 74.3        | 522    | 3  | US-09-432-335-1  | Sequence 1, Appl  |
| 3          | 514.4 | 74.3        | 522    | 4  | US-09-614-022-1  | Sequence 5, Appl  |
| 4          | 372.2 | 53.8        | 510    | 3  | US-09-130-663-5  | Sequence 5, Appl  |
| 5          | 372.2 | 53.8        | 510    | 3  | US-09-432-335-5  | Sequence 5, Appl  |
| 6          | 372.2 | 53.8        | 510    | 4  | US-09-614-022-5  | Sequence 5, Appl  |
| 7          | 145.2 | 21.0        | 525    | 2  | US-08-467-603-1  | Sequence 1, Appl  |
| 8          | 145.2 | 21.0        | 525    | 2  | US-08-466-793-1  | Sequence 1, Appl  |
| 9          | 145.2 | 21.0        | 525    | 2  | US-08-431-861A-1 | Sequence 1, Appl  |
| 10         | 78    | 11.3        | 147    | 3  | US-09-130-663-16 | Sequence 16, Appl |
| 11         | 78    | 11.3        | 147    | 3  | US-09-432-335-16 | Sequence 16, Appl |
| 12         | 78    | 11.3        | 147    | 4  | US-09-614-022-16 | Sequence 16, Appl |
| 13         | 76.2  | 11.0        | 147    | 3  | US-09-130-663-24 | Sequence 24, Appl |
| 14         | 76.2  | 11.0        | 147    | 3  | US-09-432-335-24 | Sequence 24, Appl |
| 15         | 76.2  | 11.0        | 147    | 4  | US-09-614-022-24 | Sequence 24, Appl |
| 16         | 65.4  | 9.5         | 147    | 3  | US-09-130-663-17 | Sequence 17, Appl |
| 17         | 65.4  | 9.5         | 147    | 3  | US-09-432-335-17 | Sequence 17, Appl |
| 18         | 65.4  | 9.5         | 147    | 4  | US-09-614-022-17 | Sequence 17, Appl |
| c 19       |       |             |        |    |                  |                   |
| 19         | 54    | 7.8         | 7218   | 1  | US-08-232-463-14 | Sequence 14, Appl |
| 20         | 52    | 7.5         | 52     | 3  | US-09-130-663-15 | Sequence 15, Appl |
| 21         | 52    | 7.5         | 52     | 3  | US-09-432-335-15 | Sequence 15, Appl |
| c 22       |       |             |        |    |                  |                   |
| 22         | 52    | 7.5         | 52     | 4  | US-09-614-022-15 | Sequence 15, Appl |
| 23         | 49.4  | 7.1         | 51     | 3  | US-09-130-663-19 | Sequence 19, Appl |
| 24         | 49.4  | 7.1         | 51     | 3  | US-09-432-335-19 | Sequence 19, Appl |
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| 26         | 42.4  | 6.1         | 2338   | 1  | US-08-425-069-1  | Sequence 1, Appl  |
| 27         | 42.4  | 6.1         | 2338   | 2  | US-08-317-844B-1 | Sequence 1, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-130-663-1  
Sequence 1, Application US/09130663A  
Patent No. 6020163  
GENERAL INFORMATION:  
APPLICANT: Conklin, Darrell C.  
TITLE OF INVENTION: LIPOCALIN HOMOLOG  
FILE OF INVENTION: 97-24  
CURRENT APPLICATION NUMBER: US/09/130,663A  
CURRENT FILING DATE: 1998-08-05  
EARLIER APPLICATION NUMBER: 60/054,867  
EARLIER FILING DATE: 1997-08-06  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 522  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (7)...(516)  
US-09-130-663-1

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|-----------------------|---------------------------------------------------------------|---------------------|---------------|-------------------|
| Query Match           | 74.38;                                                        | Score 514.4;        | DB 3;         | Length 522;       |
| Best Local Similarity | 99.8;                                                         | Pred. No. 1.1e-125; |               |                   |
| Matches 515;          | Conservative                                                  | 0;                  | Mismatches 1; | Indels 0; Gaps 0; |
| 39                    | CTGGAGATGAGAACCTGTCTCTGGGTGTACAGCTCGCGCTGGCGCTGCCTGTCCCTTC    | 98                  |               |                   |
| 1                     | CTGAGATGAGAACCTGTCTCTGGGTGTACAGCTCGCGCTGGCGCTGCCTGTCCCTTC     | 60                  |               |                   |
| 99                    | ACCTCTGGAGGAGGATATACAGAGGACCTGTGCTGTGAAGGCATGTGTGTCGATAG      | 158                 |               |                   |
| 61                    | ACCTCTGGAGGAGGAGATATACAGAGGACCTGTGCTGTGAAGGCATGGTGGTCGATAG    | 120                 |               |                   |
| 159                   | GACTTTCGGAGACGAGGAGGCCACGAAAGTGTGCCAGTGAAGTGACAGCCCTGGGC      | 218                 |               |                   |
| 121                   | GACTTTCGGAGACGAGGAGGCCACGAAAGTGTGCCAGTGAAGTGACAGCCCTGGGC      | 180                 |               |                   |
| 219                   | GGTGGGAAGTTGGAAGCCACCTGTCACTTCATCAGGAGGAGTGGGTGCATCCAGAGAGAA  | 278                 |               |                   |
| 181                   | GGTGGGAAGTTGGAAGCCACCTTCACCTTCATCAGGAGGAGTGGGTGCATCCAGAGAGAA  | 240                 |               |                   |
| 279                   | ATPCTTGATCGGAGACGAGGAGGACCTTGGCAAAATACAGCGCCTATGGGGGACGAAAGTC | 338                 |               |                   |
| 241                   | ATPCTTGATCGGAGACGAGGAGGACCTTGGCAAAATACAGCGCCTATGGGGGACGAAAGTC | 300                 |               |                   |
| 339                   | ATGTACTCTCAGGAGCTGCCACGAGGAGGACCACTACATCTTTTACTGCAAGAGCACCAGC | 398                 |               |                   |
| 301                   | ATGTACTCTCAGGAGCTGCCACGAGGAGGACCACTACATCTTTTACTGCAAGAGCACCAGC | 360                 |               |                   |









Db 412 GAGCAGAGCAAGAGGCTTGGAGATTTTCGGATTTCTCAAGAGCAAGGA---TTG 468  
QY 504 GAGGAGGACATTTTCAGCCCTTCAGAGGAGGAGCTGGCTTCCCGAA 551  
Db 469 AACAGAGAGATTTTGGAACTGCGCAGAGCAAACTGCTCTCCAGGA 516

RESULT 8

US-08-466-793-1  
; Sequence 1, Application US/08466793  
; Patent No. 5991716  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrey  
APPLICANT: Bizindauskas, Christine B.  
TITLE OF INVENTION: Peptides from Dog  
TITLE OF INVENTION: Allergenic Proteins and  
TITLE OF INVENTION: Peptides from Dog  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,793  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156,549  
FILING DATE: 22-NOV-1993  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..525  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 79..525  
US-08-466-793-1

Query Match 21.0%; Score 145.2; DB 2; Length 525;  
Best Local Similarity 60.0%; Pred. No. 4.3e-29;  
Matches 281; Conservative 0; Mismatches 178; Indels 9; Gaps 2;  
QY 84 GTGCGCTGCTTCACCCCTGGAGGAGGATATCAGAGGACCTGGTACGTGAGGCC 143  
Db 58 GATACCCACCCCTGGAGGAGGACACTGTGCTGTGTCAGGAATGTATCTGAGGCC 117  
QY 144 ATGGTGTGCTGATAGGACTTTCGGAGGACAGAGGCCCGCAGAGGCTGCCAGTAG 203

Db 118 ATGACACAGCAGCAGGAGGTGCTCGA-----GAGCCTGACTCAGTCCCATGATC 171  
QY 204 GTGACAGCCCTCGGCGGTGGGAAGCTTGGAGAGCCACGCTTCACTTCAATGAGGAGGATCGG 263  
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QY 264 TGCATCCAGAGAAAATCTGTATCGGAAGACGGAGAGCCTTGGCAAAATACAGAGCGCTAT 323  
Db 232 TGCCAGAACATCAGCGGTGCTCTGCAAAAACCTCTGAGCCTGGCAAAATACAGCGCATAC 291  
QY 324 GGGGCGAGGAGACTCATGTACTCTCAGAGAGCTGCCAGAGGAGGACCACTACATCTTTTAC 383  
Db 292 GAGGCGCAGCGTGTCTGTTTCATCCAGCGCTCCCGGTGAGGAGCACCACACTTCTCTAC 351  
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QY 444 GATACCAACCGGAGGAGCCCTGGAGAAATTTAAGAAATGTGTGCGAGCGCAGAGGATCTCG 503  
Db 412 GAGCAGAGCAAGAGCGCTTGGAGGATTTTCGGGAATCTCAAGAGCCAAAGGA---TTG 468  
QY 504 GAGGAGGACATTTTCAGCCCTCTCAGAGCGGAAAGCTGCGTTTCCCGAA 551  
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RESULT 9

US-08-491-861A-1  
; Sequence 1, Application US/08491861A  
; Patent No. 5939283  
GENERAL INFORMATION:  
APPLICANT: Morgenstern, Jay P.  
APPLICANT: Kanieczny, Andrey  
APPLICANT: Bizindauskas, Christine B.  
APPLICANT: Brauer, Andrew W.  
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
TITLE OF INVENTION: Dander and Uses Thereof  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,861A  
FILING DATE: 27-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/999,712  
FILING DATE: 31-Dec-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 525 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA



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Qy 139 AGCCATGCTGGTCGATGAAGACTTT 164  
Db 122 AGCCATGCTGGTCGATGAAGACTTT 147

RESULT 13  
US-09-130-663-24  
; Sequence 24, Application US/09130663A  
; Patent No. 6020163  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/130,663A  
; CURRENT FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Flag linker  
US-09-130-663-24

Query Match 11.0%; Score 76.2; DB 3; Length 147;  
Best Local Similarity 96.3%; Pred. No. 3.1e-11;  
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 84 GCTGCCCTGCTCCCTCACCTGGAGGAGGAGGATATCACAGGACCTGGTACGTGAAGGCC 143  
Db 67 GGTGCTGCTGCTCCCTCACCTGGAGGAGGAGGATATCACAGGACCTGGTACGTGAAGGCC 126  
Qy 144 ATGGTGGTCGATGAAGACTTT 164  
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; Sequence 24, Application US/09432335  
; Patent No. 6143720  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/432,335  
; CURRENT FILING DATE: 1999-11-02  
; EARLIER APPLICATION NUMBER: 09/130,663  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/054,867  
; EARLIER FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Flag linker  
US-09-432-335-24

Query Match 11.0%; Score 76.2; DB 3; Length 147;  
Best Local Similarity 96.3%; Pred. No. 3.1e-11;  
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 84 GCTGCCCTGCTCCCTCACCTGGAGGAGGAGGATATCACAGGACCTGGTACGTGAAGGCC 143

Db 67 GGTGCTGCTGCTCCCTCACCTGGAGGAGGAGGATATCACAGGACCTGGTACGTGAAGGCC 126  
Qy 144 ATGGTGGTCGATGAAGACTTT 164  
Db 127 ATGGTGGTCGATGAAGACTTT 147

RESULT 15  
US-09-614-022-24  
; Sequence 24, Application US/09614022  
; Patent No. 6365716  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: LIPOCALIN HOMOLOG  
; FILE REFERENCE: 97-24  
; CURRENT APPLICATION NUMBER: US/09/614,022  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 09/130,663  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/054,867  
; PRIOR FILING DATE: 1997-08-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Flag linker  
US-09-614-022-24

Query Match 11.0%; Score 76.2; DB 4; Length 147;  
Best Local Similarity 96.3%; Pred. No. 3.1e-11;  
Matches 78; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 84 GCTGCCCTGCTCCCTCACCTGGAGGAGGAGGATATCACAGGACCTGGTACGTGAAGGCC 143  
Db 67 GGTGCTGCTGCTCCCTCACCTGGAGGAGGAGGATATCACAGGACCTGGTACGTGAAGGCC 126  
Qy 144 ATGGTGGTCGATGAAGACTTT 164  
Db 127 ATGGTGGTCGATGAAGACTTT 147

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Job time : 55.2996 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 21:14:50 ; Search time 53.348 Seconds  
(without alignments)  
6148.496 Million cell updates/sec

Title: US-09-099-823-5  
Perfect score: 692  
Sequence: 1 GAGCCCACTGACCTGCCGA.....ATTAAGTCCTTCGCCCA 692

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2\_5/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_5/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_5/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_5/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_5/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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13: /cgn2\_5/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_5/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query % | Score Match | Length | DB ID | Description        |
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| 2          | 692     | 100.0       | 692    | 10    | US-09-099-823-5    |
| 3          | 514.4   | 74.3        | 523    | 10    | US-09-351-845-1    |
| c 4        | 493.6   | 69.9        | 501    | 10    | US-09-833-381-803  |
| c 5        | 337     | 48.7        | 337    | 10    | US-09-099-823-3    |
| 6          | 296     | 42.8        | 336    | 10    | US-09-833-381-1747 |
| 7          | 245     | 35.4        | 245    | 10    | US-09-099-823-2    |
| 8          | 236     | 34.1        | 236    | 10    | US-09-099-823-1    |
| 9          | 145.2   | 21.0        | 525    | 10    | US-09-374-671-1    |
| 10         | 54.8    | 7.9         | 555    | 9     | US-10-143-576-1    |
| 11         | 54.8    | 7.9         | 555    | 10    | US-09-854-847-1    |
| 12         | 54.8    | 7.9         | 579    | 10    | US-09-854-847-9    |
| 13         | 54.8    | 7.9         | 597    | 10    | US-09-854-847-17   |
| 14         | 53.2    | 7.7         | 762    | 9     | US-10-028-072-237  |
| 15         | 53.2    | 7.7         | 762    | 9     | US-10-121-049-237  |
| 16         | 53.2    | 7.7         | 762    | 9     | US-10-123-904-237  |
| 17         | 53.2    | 7.7         | 762    | 9     | US-10-140-470-237  |
| 18         | 48      | 6.9         | 432    | 10    | US-09-854-847-25   |
| 19         | 46      | 6.6         | 570    | 10    | US-09-800-729-37   |
|            |         |             |        |       | Sequence 4, Appli  |
|            |         |             |        |       | Sequence 5, Appli  |
|            |         |             |        |       | Sequence 1, Appli  |
|            |         |             |        |       | Sequence 803, App  |
|            |         |             |        |       | Sequence 3, Appli  |
|            |         |             |        |       | Sequence 1747, Ap  |
|            |         |             |        |       | Sequence 2, Appli  |
|            |         |             |        |       | Sequence 1, Appli  |
|            |         |             |        |       | Sequence 1, Appli  |
|            |         |             |        |       | Sequence 1, Appli  |
|            |         |             |        |       | Sequence 9, Appli  |
|            |         |             |        |       | Sequence 17, Appli |
|            |         |             |        |       | Sequence 237, App  |
|            |         |             |        |       | Sequence 237, App  |
|            |         |             |        |       | Sequence 237, App  |
|            |         |             |        |       | Sequence 25, Appli |
|            |         |             |        |       | Sequence 37, Appli |

|      |      |     |      |    |                     |
|------|------|-----|------|----|---------------------|
| c 20 | 40   | 5.8 | 948  | 10 | US-09-886-055-194   |
| 21   | 38.2 | 5.5 | 284  | 10 | US-09-878-574-11281 |
| 22   | 38.2 | 5.5 | 239  | 10 | US-09-878-574-11878 |
| 23   | 38.2 | 5.5 | 385  | 10 | US-09-878-574-59    |
| 24   | 38.2 | 5.5 | 391  | 10 | US-09-878-574-2305  |
| 25   | 38.2 | 5.5 | 504  | 10 | US-09-878-574-4330  |
| 26   | 38.2 | 5.5 | 1914 | 10 | US-09-815-242-7960  |
| 27   | 37.6 | 5.4 | 1852 | 10 | US-09-969-852-4     |
| c 28 | 36.8 | 5.3 | 576  | 9  | US-09-938-842A-1855 |
| 29   | 36.6 | 5.3 | 320  | 10 | US-09-923-876-3670  |
| 30   | 36.4 | 5.3 | 2602 | 10 | US-09-917-800A-1590 |
| 31   | 36.2 | 5.2 | 3502 | 10 | US-09-880-192-37    |
| c 32 | 36   | 5.2 | 1464 | 9  | US-10-166-359-1     |
| c 33 | 36   | 5.2 | 1464 | 9  | US-10-166-113-1     |
| c 34 | 36   | 5.2 | 1464 | 9  | US-10-166-357-1     |
| c 35 | 36   | 5.2 | 1464 | 9  | US-10-166-372-1     |
| c 36 | 36   | 5.2 | 1464 | 10 | US-09-149-045-1     |
| 37   | 36   | 5.2 | 5515 | 10 | US-09-751-100B-98   |
| c 38 | 35.8 | 5.2 | 2379 | 10 | US-09-615-242-7888  |
| c 39 | 35.8 | 5.2 | 3698 | 9  | US-09-945-901-43    |
| c 40 | 35.8 | 5.2 | 3698 | 9  | US-10-007-747-43    |
| c 41 | 35.8 | 5.2 | 3698 | 9  | US-10-038-937-43    |
| c 42 | 35.8 | 5.2 | 4002 | 9  | US-09-945-901-53    |
| c 43 | 35.8 | 5.2 | 4002 | 9  | US-10-007-747-53    |
| c 44 | 35.8 | 5.2 | 4002 | 9  | US-10-038-937-53    |
| c 45 | 35.8 | 5.2 | 4017 | 9  | US-09-945-901-49    |

## ALIGNMENTS

## RESULT 1

US-09-099-823-4  
; Sequence 4, Application US/09099823  
; Patent No. US0020018990A1  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KASS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: SCHEFFEL, CHRISTI  
; APPLICANT: STROUPE, STEPHEN D.  
; APPLICANT: YU, HONG  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/099,823  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/879,354  
; FILING DATE: 20-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.

Sequence 194, Appl  
Sequence 11281, A  
Sequence 11878, A  
Sequence 59, Appl  
Sequence 2305, Ap  
Sequence 4330, Ap  
Sequence 7960, Ap  
Sequence 4, Appli  
Sequence 1855, Ap  
Sequence 3670, Ap  
Sequence 1590, Ap  
Sequence 37, Appl  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 98, Appl  
Sequence 7868, Ap  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 53, Appl  
Sequence 53, Appl  
Sequence 53, Appl  
Sequence 49, Appl



|    | Query Match           | 74.38;                                                         | Score 514.4;        | DB 10;    | Length 523; |
|----|-----------------------|----------------------------------------------------------------|---------------------|-----------|-------------|
|    | Best Local Similarity | 99.88;                                                         | Pred. No. 1.1e-126; |           |             |
|    | Matches 515;          | Conservative 0;                                                | Mismatches 1;       | Indels 0; | Gaps        |
| QY | 39                    | CTFGAGATGAGACACCTCTTCGGGTGTCAAGCTGGGCTGGCCGTGGCTTCCTTC         | 98                  |           |             |
| Db | 2                     | CTFGAGATGAGACCTGTCTGGGTGTCAAGCTGGGCTGGCCGTGGCTTCCTTC           | 61                  |           |             |
| QY | 99                    | ACCTCTGGAGGAGGAGGATATACAGGAGCCTGTGTAGTGAAGGCCATGGTGGTGCATAAG   | 158                 |           |             |
| Db | 62                    | ACCTCTGGAGGAGGAGGATATACAGGAGCCTGTGTAGTGAAGGCCATGGTGGTGCATAAG   | 121                 |           |             |
| QY | 159                   | GACTTTCCGAGGACAGSAGGCCACGAGGAAGTGTCCCATGTGAAGGTGACAGACCCCTGGGC | 218                 |           |             |
| Db | 122                   | GACTTTCCGAGGACAGSAGGCCACGAGGAAGTGTCCCATGTGAAGGTGACAGACCCCTGGGC | 181                 |           |             |
| QY | 219                   | GGTGGGAAGTTGGAAGCCACAGCTTCACCTTCATGAGGGAGGATCGTGTGCATCCAGAGAAA | 278                 |           |             |
| Db | 182                   | GGTGGGAAGTTGGAAGCCACAGCTTCACCTTCATGAGGGAGGATCGTGTGCATCCAGAGAAA | 241                 |           |             |

|     |    |                                                                 |     |
|-----|----|-----------------------------------------------------------------|-----|
| 189 | QY | GTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAAGCCAGGTCACCTTC      | 248 |
| 501 | Db | GTGTCCCCAGTGAAGGTGACAG-CCTTGGCTGTGGGAAGTTGAAGCCAGGTCACCTTC      | 443 |
| 249 | QY | ATGAGGAGGATCGGTGCATCCAGAAAGAAATCCTGATCGGGAAGACGGAGGAGCCTGGC     | 308 |
| 442 | Db | ATGAGGAGGATGTGTCATCCAGAAAGAAATCCTGATCGGGAAGACGGAGGAGCCTGGC      | 363 |
| 309 | QY | AAATACAGCCCTATGTGGGCGAGGACATCATGTACTGTCAGAGAGCTGCCACGAGGGAC     | 368 |
| 382 | Db | AAATACAGCCCTATGTGGGCGAGGAGCTCATGTACTGTCAGAGAGCTGCCACGAGGGAC     | 323 |
| 369 | QY | CACATACATCTTTTACTTCAAAAGACCAACCATGTGGGGCCCTGCTCCACATGGGAAGCTT   | 428 |
| 322 | Db | CACATACATCTTTTACTTCAAAAGACCAACCATGTGGGGCCCTGCTCCACATGGGAAGCTT   | 263 |
| 429 | QY | GTGGGTAGGAATTTGATATACCAACCGGAGGCGCCCTGGGAAGAATTTAAGAAATTTGGTCAG | 488 |
| 262 | Db | GTGGGTAGGAATTTGATATACCAACCGGAGGCGCCCTGGGAAGAATTTAAGAAATTTGGTCAG | 203 |
| 489 | QY | CGCAGAGGACTCTCGGAGGAGGACATTTTCAAGCCCTGTCAGACGGGAGCTCGCTCC       | 548 |
| 202 | Db | CGCAGAGGACTCTCGGAGGAGGACATTTTCAAGCCCTGTCAGACGGGAGCTCGCTCC       | 143 |
| 549 | QY | GAACACT'AGGCAGCCCCGGGTCTGCACCTCCAGAGCCACCTACCACACAGACACAG       | 608 |
| 142 | Db | GAACACT'AGGCAGCCCCGGGTCTGCACCTCCAGAGCCACCTACCACACAGACACAG       | 83  |





Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-SEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120.US.P1  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 245 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-099-823-2  
Query Match 35.4%; Score 245; DB 10; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1.1e-35;  
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 113 GATATCATCAGGACCTGCTGAGGCCATGCTGCTGATGAGGACTTTCGGGAGGA 172  
DB 1 GATATCATCAGGACCTGCTGAGGCCATGCTGCTGATGAGGACTTTCGGGAGGA 60  
QY 173 CAGGAGGCCAGGAGGTGTCCCGAGGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGA 232  
DB 61 CAGGAGGCCAGGAGGTGTCCCGAGGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGA 120  
QY 233 AGCCACCTTTCACCTTCATCAGGAGGATGCTGATCCAGAGAGAAATCCTGATGGGAA 292  
DB 121 AGCCACCTTTCACCTTCATCAGGAGGATGCTGATCCAGAGAGAAATCCTGATGGGAA 180  
QY 293 GACGAGGAGCTTGGCAATACAGGCGCTATGGGCGCAGGAGCTATGACTGCGAGGA 352  
DB 181 GACGAGGAGCTTGGCAATACAGGCGCTATGGGCGCAGGAGCTATGACTGCGAGGA 240

QY 353 GCTGC 357  
DB 241 GCTGC 245  
RESULT 8  
US-09-099-823-1  
Sequence 1, Application US/09099823  
Patent No. US20020018990A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-SEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120.US.P1  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-099-823-1  
Query Match 34.1%; Score 236; DB 10; Length 236;  
Best Local Similarity 100.0%; Pred. No. 2.5e-53;  
Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACGCCCTGACCTGCTGCGGAGTGGCAGCAGAGCTCTGAGATGAGACCTCTTCC 60  
DB 1 GACGCCCTGACCTGCTGCGGAGTGGCAGCAGAGCTCTGAGATGAGACCTCTTCC 60  
QY 61 TGGGTGTACCTCGGCTGCGGCGCTGCGGCTGCTTACCTTGGAGGAGGATATCA 120  
DB 61 TGGGTGTACCTCGGCTGCGGCGCTGCGGCTGCTTACCTTGGAGGAGGATATCA 120

QY 121 CAGGACCTGTGTACGTGAAGCCATCGTGTGATAGGACTTTCCGAGGACAGAGGC 180  
Db 121 CAGGACCTGTGTACGTGAAGCCATCGTGTGATAGGACTTTCCGAGGACAGAGGC 180  
QY 181 CCAGGAAGTGTCCCGACGTGAAGCTGACAGCCCTGGCGGTGGGAGTGTGGAAGCC 236  
Db 181 CCAGGAAGTGTCCCGACGTGAAGCTGACAGCCCTGGCGGTGGGAGTGTGGAAGCC 236

## RESULT 9

US-09-374-671-1  
; Sequence 1, Application US/09374671  
; Patent No. US20020012963A1  
; GENERAL INFORMATION:  
; APPLICANT: Morgenstern, Jay P.  
; APPLICANT: Kanleczny, Andrey  
; APPLICANT: Bizindaukas, Christine B.  
; APPLICANT: Brauer, Andrew W.  
; TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
; TITLE OF INVENTION: Dander and Uses Therefor  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/374,671  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/491,861  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; LENGTH: 525 base pairs  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..525  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 79..525  
US-09-374-671-1

Query Match 21.0%; Score 145.2; DB 10; Length 525;  
Best Local Similarity 60.0%; Pred. No. 2.9e-29;  
Matches 281; Conservative 0; Mismatches 178; Indels 9; Gaps 2;

QY 84 GCTGCTCTCTCTACCTGAGGAGGAGATATACAGGAGGAGCTGTGACGTGAAGGCC 143  
Db 58 GATACCCAGCCCTTGGGAAGGACACTGTGGCTGTGTCAGGGAATGTGTCTGAAGGCC 117  
QY 144 ATGTGTGTGTAAGGACTTTCCGAGGACAGGAGGCCAGGAAGGTGTCCCAAGTGAAG 203  
Db 118 ATGACAGACAGACAGGAGGTGCTGCA-----GAAGCTGACTGACTGCTCCATGATC 171

QY 204 GTGACAGCCCTGCGGGTGGGAAGTTGAAGCCACGCTTACCTTCATGAGGAGGAGTCCG 263  
Db 172 CTCGAAGCCCGAGAGAGGGGCAACCTCGAAGCCAGATCACAGCTGACAAATGGCTAG 231  
QY 264 TGCATCCAGAGAGAAATCTGTGTCGCGAAGCAGGAGAGCTTGGCAAAACAGAGCCCTAT 323  
Db 232 TGCAGACATCATCGGTGCTGTGCRAAAACCTCTGAGCTTGGCAATACAGGCATAC 291  
QY 324 GGGGCGAGGAGCTCATGTACTGACAGAGCTGCCAGAGGAGGACCACTACATCTTTTAC 383  
Db 292 GAGGGCCAGCGGTGTCTGTTCATCCAGCGTCCCGGTGAGGGACCACTACATCTTCTAC 351  
QY 384 TCGAAGACCCAGCACCACATGGGGGCTCTCCACATGGGAAAGCTTGTGGTGAATCT 443  
Db 352 TCGAGAGGCGAGCTCCATGGGAGGAGATCCGAATGGCAAGCTTCTGGGAAGGATCT 411  
QY 444 GATACCAACCGGAGGCGCTTGGGAAGATTTAAGAAATTTGTCAGCGCAGGAGCTCTCG 503  
Db 412 GAGCAGAGCCCAAGAGCGCTTGGAGGATTTTCGGGAATTTCTCAAGAGCAAGGA--TTG 468  
QY 504 GAGGAGACATTTTTCAGCGCCCTGACAGCGGAGAGCTGGTTCCTCCGAA 551  
Db 469 ACCAGAGAGATTTTGGACTCCCGCAGAGGAACCTGCTCTCCAGGA 516

## RESULT 10

US-10-143-576-1  
; Sequence 1, Application US/10143576  
; Publication No. US20030013151A1  
; GENERAL INFORMATION:  
; APPLICANT: HU, Song et al.  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001237  
; CURRENT APPLICATION NUMBER: US/10/143,576  
; CURRENT FILING DATE: 2002-05-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-143-576-1

Query Match 7.9%; Score 54.8; DB 9; Length 555;  
Best Local Similarity 46.6%; Pred. No. 2.1e-05;  
Matches 247; Conservative 0; Mismatches 277; Indels 6; Gaps 2;

QY 45 ATGAAGACCTCTCTCTGTTGTGTCAGCTGCGGCTGCGCGCTGCGCTTCCTTCACCCCTG 104  
Db 25 ATCTGACCTCTCTCTGCGGCGCCACAGGCTCAGGCTGAGGTTCTGTGACGCTGACTTC 84  
QY 105 GAGGAGGAGATATACAGGAGCCTGTGTACTGTGAAGGCCATGG---TGTGTAAGAGAC 161  
Db 85 AATGCTGAAAGTTCTCAGGCTCTGTGTACTGTCTCTCATGGCATCTGACTGCAGGGTTC 144  
QY 162 TTTCCGAGGACAGGAGGCCAGAGAGGTGTCCTCCAGTGAAGGTGACAGCCCTGGGCGGT 221  
Db 145 TTCTTGGCAGAGAGGACCACTGTCCATGTCCACAGGGGCCATCAGGCCACAGAGAG 204  
QY 222 GGGAGTGTGGAGCCAGCTTACCTTCATGAGGAGAGATCGGTGTGTCATCCAGAGAAATC 281  
Db 205 GCGGCGCTCCAGCTCCATGAGTGTCCCGGCGGAGGAGCTGTAAACAGGTGGATGCC 264  
QY 282 CTGATCGGGAAGCGGAGAGCCCTGGCAAAATACAGGCGCTATG---GGGGCAGGAAGCTC 338  
Db 265 GAGTACTCTGAAGTGGGCTCCGAGGGGACACTTCAGAGTCCCGGCTTGGGCTACCTGGAC 324  
QY 339 ATGTACTCTCAGGAGTGTCCCAAGGAGGAGCACTTACATCTTTTACTGCAAAAGCAGCAC 398  
Db 325 GTGGCATCTGTGACAGACTACAGTCTCTTCCGCTCTTTTACATCTACAGGAGCTG 384









GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:05:30 ; Search time 1923.58 Seconds  
(without alignments)  
5826.269 Million cell updates/sec

Title: US-09-099-823-5

Perfect score: 692  
Sequence: 1 GAGCCGAGTGAAGTGGCGA.....ATTAAGTCTTCTCCCGCGA 692

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST.\*

1: em\_estha.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estnu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hic.\*

9: gb\_estl.\*

10: gb\_estl2.\*

11: gb\_hic.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: gb\_gss.\*

18: em\_gss\_hum.\*

19: em\_gss\_inv.\*

20: em\_gss\_pln.\*

21: em\_gss\_vit.\*

22: em\_gss\_fun.\*

23: em\_gss\_mam.\*

24: em\_gss\_mus.\*

25: em\_gss\_other.\*

26: em\_gss\_pro.\*

27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| C 1        | 499   | 72.1        | 532    | 10 AW513637 | AW513637 x047110.x |
| C 2        | 465   | 67.2        | 513    | 9 AA977608  | AA977608 oncle03.s |
| C 3        | 460.6 | 66.6        | 477    | 9 AI251747  | AI251747 qn90f12.x |
| C 4        | 452.8 | 65.4        | 499    | 9 AI219510  | AI219510 qn24d02.x |
| C 5        | 410.4 | 59.3        | 415    | 9 AA460385  | AA460385 xz51e06.r |
| C 6        | 375   | 54.2        | 431    | 9 AA936288  | AA936288 on75f11.s |

|      |       |      |      |             |                    |
|------|-------|------|------|-------------|--------------------|
| C 7  | 337   | 48.7 | 337  | 9 AA460323  | AA460323 xz51e06.s |
| C 8  | 329.2 | 47.6 | 349  | 9 AI143970  | AI143970 qe10c11.k |
| C 9  | 171.2 | 24.7 | 603  | 10 BB618259 | BB618259 BB61829   |
| C 10 | 169.6 | 24.5 | 626  | 10 BB028765 | BB028765 BB028765  |
| C 11 | 162.2 | 23.4 | 519  | 9 AI877465  | AI877465 ud10d09.r |
| C 12 | 156.4 | 22.6 | 494  | 14 RA7029   | RA7029 Y358 Rat in |
| C 13 | 148   | 21.4 | 337  | 12 BF193883 | BF193883 245614 MA |
| C 14 | 146   | 21.1 | 594  | 10 AW920286 | AW920286 EST331590 |
| C 15 | 119.8 | 17.3 | 501  | 10 AW049121 | AW049121 UI-M-BH1- |
| C 16 | 98.4  | 14.2 | 462  | 13 BM087898 | BM087898 500754 MA |
| C 17 | 82    | 11.8 | 438  | 12 BF603580 | BF603580 269132 MA |
| C 18 | 55.4  | 8.0  | 518  | 12 BG814151 | BG814151 daf64a03. |
| C 19 | 53.8  | 7.8  | 312  | 9 AA851021  | AA851021 EST193789 |
| C 20 | 53.4  | 7.7  | 454  | 12 BF405590 | BF405590 UI-R-CAL- |
| C 21 | 51    | 7.4  | 322  | 12 BF288401 | BF288401 EST452992 |
| C 22 | 50.8  | 7.3  | 513  | 12 BF403655 | BF403655 UI-R-CAL- |
| C 23 | 48.4  | 7.0  | 521  | 12 BF404046 | BF404046 UI-R-CAL- |
| C 24 | 47.6  | 6.9  | 1020 | 17 CNS03R58 | AL256805 Tetradon  |
| C 25 | 47.4  | 6.8  | 426  | 10 AW158517 | AW158517 z42c10.x  |
| C 26 | 47.4  | 6.8  | 427  | 10 AW158842 | AW158842 z42c10.x  |
| C 27 | 46.4  | 6.7  | 571  | 12 BF396144 | BF396144 UI-R-CAL- |
| C 28 | 45.8  | 6.6  | 758  | 17 BH359934 | BH359934 CH230-126 |
| C 29 | 45.4  | 6.6  | 618  | 13 BJ045011 | BJ045011 BJ045011  |
| C 30 | 45.2  | 6.5  | 356  | 10 BE481242 | BE481242 166614 BA |
| C 31 | 45    | 6.5  | 742  | 13 BI520644 | BI520644 603071606 |
| C 32 | 44.6  | 6.4  | 494  | 14 B0032434 | B0032434 UI-1-CF0- |
| C 33 | 44.4  | 6.4  | 910  | 17 CNS0060N | AL065629 Drosophil |
| C 34 | 44.2  | 6.4  | 339  | 14 B0461044 | B0461044 HE01G01r  |
| C 35 | 44.2  | 6.4  | 417  | 14 N68123   | N68123 Yz54ell.sl  |
| C 36 | 44.2  | 6.4  | 551  | 14 B0469025 | B0469025 HM03C09r  |
| C 37 | 44.2  | 6.4  | 576  | 14 B0463781 | B0463781 HG01G16r  |
| C 38 | 44.2  | 6.4  | 647  | 13 BI954086 | BI954086 HYSME001  |
| C 39 | 44.2  | 6.4  | 663  | 13 BI957662 | BI957662 HYSME001  |
| C 40 | 44.2  | 6.4  | 805  | 12 BP267509 | BP267509 HV CBA001 |
| C 41 | 44.2  | 6.4  | 820  | 12 BF265032 | BF265032 HV CBA001 |
| C 42 | 44.2  | 6.4  | 847  | 13 BI953680 | BI953680 HYSME001  |
| C 43 | 44.2  | 6.4  | 875  | 12 BF267309 | BF267309 HV CBA001 |
| C 44 | 44    | 6.4  | 538  | 9 AL588422  | AL588422 AL588422  |
| C 45 | 44    | 6.4  | 581  | 9 AL588768  | AL588768 AL588768  |

## ALIGNMENTS

RESULT 1  
AW513637/C

LOCUS

DEFINITION

similar to FR:063613 Q63613 ODORANT-BINDING PROTEIN. ; mRNA

sequence.

AW513637

AW513637.1 GI:7151715

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

532 bp mRNA linear EST 03-MAR-2000  
x047110.x1 NCI-CGAP Dtl Homo sapiens cDNA clone IMAGE:2707171 3'  
similar to FR:063613 Q63613 ODORANT-BINDING PROTEIN. ; mRNA  
sequence.  
AW513637  
AW513637.1 GI:7151715  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 532)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emert-Buck, M.D., Ph.D.  
CGAP Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
Clone Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)





## RESULT 3

AI251747/c  
LOCUS AI251747 477 bp mRNA linear EST 05-NOV-1998  
DEFINITION qn9012.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1854287 3' similar to TR:063613 063613 ODORANT-BINDING  
PROTEIN. ;, mRNA sequence.  
AI251747  
ACCESSION AI251747.1 GI:3848276  
VERSION AI251747.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 477)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40UP from Gibco  
High quality sequence stop: 396.

## FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1854287"  
/lab\_host="Soares\_NFL\_T\_GBC\_S1"  
/lab\_host="DH108"  
/notes="Organ: pooled; Vector: pFT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NET, and B-cell  
NCI-CGAP GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 79 a 123 c 145 g 130 t  
ORIGIN

Query Match 66.6%; Score 460.6; DB 9; Length 477;  
Best Local Similarity 99.1%; Pred. No. 4.9e-101;  
Matches 463; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 226 AGTTGAGGACGCTTCACTTATGAGGAGGATGCTGATCCAGAGAAATCTGGA 285  
DB 476 AGTTGAGGACGCTTCACTTATGAGGAGGATGCTGATCCAGAGAAATCTGGA 417  
QY 286 TCGGAGAGCGGAGGACCTGCCAATACAGCGCTATGGGGGCGAGAGCTCATGTACC 345  
DB 416 TCGGAGAGCGGAGGAGCTTGGCAATACAGCGCTATGGGGGCGAGAGCTCATGTACC 357  
QY 346 TCGAGAGCTGCCAGGAGGAGGACCATCATCTTTTACTGCAAGACGACCATGGGG 405  
DB 356 TCGAGGAGCTGCCAGGAGGAGGACCATCATCTTTTACTGCAAGACGACCATGGGG 297  
QY 406 GCGTCTCCACATGGAAGAGCTTGTGGTAGGAATCTGATACCAACCGGGAGCGCCCTGG 465  
DB 296 GCGTCTCCACATGGAAGAGCTTGTGGTAGGAATCTGATACCAACCGGGAGCGCCCTGG 237  
QY 466 AAGATTTAAGAAATGTTGACGAGCGAGGAGCTCTCGGAGGAGGACATTTTCACGCC 525  
DB 236 AAGATTTAAGAAATGTTGACGAGCGAGGAGCTCTCGGAGGAGGACATTTTCACGCC 177  
QY 526 TCGAGAGCGGAGAGCTGCTGCCGAGACTAGGACGAGCCCGGGCTGCACCTCCAGAC 585

DB 176 TCGAGAGCGGAGAGCTGGTCTCCGAGACTAGGACGAGCCCGGGCTGCACCTCCAGAGC 117  
QY 586 CCACCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 645  
DB 116 CCACCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 57  
QY 646 TCCCTGCTCCACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 692  
DB 56 TCCCTGCTCCACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 10  
RESULT 4  
AI219510/c  
LOCUS AI219510 499 bp mRNA linear EST 30-NOV-1998  
DEFINITION qn24402.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1845603 3' similar to TR:063613 063613 ODORANT-BINDING  
PROTEIN. ;, mRNA sequence.  
AI219510  
ACCESSION AI219510.1 GI:3801713  
VERSION AI219510.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 499)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 536 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 330.  
Location/Qualifiers  
1..499  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1845603"  
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/lab\_host="DH108"  
/notes="Organ: pooled; Vector: pFT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NET, and B-cell  
NCI-CGAP GCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 85 a 135 c 151 g 126 t  
ORIGIN

Query Match 65.4%; Score 452.8; DB 9; Length 499;  
Best Local Similarity 94.2%; Pred. No. 3.8e-99;  
Matches 469; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
QY 195 CCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAGCCAGCTTCACCTTCATGAG 254  
DB 499 CCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAGCCAGCTTCACCTTCATGAG 440  
QY 255 GAGGATCGGTGATCAGAGAAATCTGATCGGAGAGGAGGAGGCTGGCAATATAC 314  
DB 439 GAGGATCGGTGATCAGAGAAATCTGATCGGAGAGGAGGAGGCTGGCAATATAC 380  
QY 315 AGCCGCTATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 374



Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19w, testis NHT, and B-cell NCI CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 73 a 111 c 136 g 110 t 1 others  
ORIGIN

Query Match 54.2%; Score 375; DB 9; Length 431;  
Best Local Similarity 94.7%; Pred. No. 2.3e-80;  
Matches 409; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 261 CGGTGATCCAGAGAAATTCCTGATCGGAAGACGAGGAGCTGCGCAATACAGCGCC 320  
DB 431 CGGTGATCCAGAGAAATTCCTGATCGGAAGACGAGGAGCTGCGCAATACAGCGCC 372

QY 321 TATGGGGCAGGAGCTCATGTACTCTGAGGAGCTGCCAGAGGAGGACCACTACATCTT 380  
DB 371 TATGGGGCAGGAGCTCATGTACTCTGAGGAGCTGCCAGAGGAGGACCACTACATCTT 313

QY 381 TACTCTCAAGACGACCACTATGGGGCTGCTCCACATGGAAGAGCTTGTGGGTAGGAAT 440  
DB 312 TACTCTCAAGACGACCGCT-GGGGCTGCTGCTACATGGAAGAGCTTGTGGGTAGGAAT 254

QY 441 TCTGATACCAACCGGAGGCTCTGGAAGATTGAAGATTGCTGACGCAAGGAGCTC 500  
DB 253 CTTATACCAACCGGAGGCTCTGGAAGATTGAAGATTGCTGACGCAAGGAGCTC 194

QY 501 TGGAGAGGACATTTTCAGGCGCTCGAGAGGAGGAGCTGCTGCCAGACATAGCA 560  
DB 193 TGGAGAGGACATTTTCAGGCGCTCGAGAGGAGGAGCTGCTGCCAGACATAGCA 134

QY 561 GCGCCGGGTCTGCACTCCAGAGCCACCTTACACAGACAGACAGAGCGGACACCT 620  
DB 133 GCGCCGGGTCTGCACTCCAGAGCCACCTTACACAGACAGACAGAGCGGACACCT 74

QY 621 GGACTACCTCCAGCATGACCTTCCCTGCTCCACCCACCTGACTCCAAATAAGTC 680  
DB 73 GGACTACCTCCAGCATGACCTTCCCTGCTCCACCCACCTGACTCCAAATAAGTC 14

QY 681 CTTCTCCGCCCA 692  
DB 13 CTTCTCCGCCCA 2

RESULT 7  
AA460323/c 337 bp mRNA linear EST 09-JUN-1997  
LOCUS z551a06.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:795778  
DEFINITION 3' similar to TR:G207551 G207551 ODORANT-BINDING PROTEIN. ; mRNA

QY 681 CTTCTCCGCCCA 692  
DB 13 CTTCTCCGCCCA 2

QY 681 CTTCTCCGCCCA 692  
DB 13 CTTCTCCGCCCA 2

QY 681 CTTCTCCGCCCA 692  
DB 13 CTTCTCCGCCCA 2

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
Seq primer: -41m13 fwd. RT from Amersham  
High quality sequence stop: 323.

FEATURES  
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/organism="Homo sapiens"  
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/clone="IMAGE:795778"  
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/sex="male"  
/lab\_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGTGGAGCGGCCCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 57 a 80 c 119 g 81 t  
ORIGIN

Query Match 48.7%; Score 337; DB 9; Length 337;  
Best Local Similarity 100.0%; Pred. No. 3.4e-71;  
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 CTGCGCAGAGGAGGACCTACATCTTTTACTGCAAGACGAGCAGCAGCAGGCGCTGCTC 413  
DB 337 CTGCGCAGAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 278

QY 414 CACATGGAAGAGCTTGTGGTGAAGATCTGATACCAACCGGAGGCGCTGGAAGAATTT 473  
DB 277 CACATGGAAGAGCTTGTGGTGAAGATCTGATACCAACCGGAGGCGCTGGAAGAATTT 218

QY 474 AAGAAATGCTGACGCAAGGAGCTCTGGAGGAGGACATTTTCAGCGCCCTCGAGAG 533  
DB 217 AAGAAATGCTGACGCAAGGAGCTCTGGAGGAGGACATTTTCAGCGCCCTCGAGAG 158

QY 534 GGAAGCTGCTTCCCGCAACCTTAGGAGCGCCCGGGTCTGCACCTCCAGAGCCACCCCTA 593  
DB 157 GGAAGCTGCTTCCCGCAACCTTAGGAGCGCCCGGGTCTGCACCTCCAGAGCCACCCCTA 98

QY 594 CCACGACAGACAGCGCGGACCTGACCTGACCTCCAGCAGCAGCAGCAGCAGCAGCAGCAG 653  
DB 97 CCACGACAGACAGCGCGGACCTGACCTGACCTCCAGCAGCAGCAGCAGCAGCAGCAG 38

QY 654 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690  
DB 37 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1

RESULT 8  
A1143970/c 349 bp mRNA linear EST 28-SEP-1998  
LOCUS qe01c11.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:173716  
DEFINITION 3' similar to TR:Q63613 Q63613 ODORANT-BINDING PROTEIN. ; mRNA

QY 654 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690  
DB 37 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1

QY 654 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690  
DB 37 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1

QY 654 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690  
DB 37 CCACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1













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BASE COUNT 112 a 109 c 123 g 157 t
ORIGIN
TAG_SEQ=CATGG*
Query Match 17.3%; Score 119.8; DB 10; Length 501;
Best Local Similarity 60.1%; Pred. No. 1.2e-18;
Matches 235; Conservative 0; Mismatches 152; Indels 4; Gaps 2;
QY 246 TTCATGAGGAGATCGGTGCTATCCAGAGAAATCTGATCGGAAGAGGGAGGAGCTT 305
Db 497 TTCTGACAAATGGTCAATTCGCGTGAATTTTAAATTCGTGATGAAGAAACAGAGAGCTT 438
QY 306 GGCATAATACAGCGCTATGGGGCGAGAGCTCATGTACTCTCAGGAGCTGCCAGGAGG 365
Db 437 GGCATAATACAGCGCTTTCATTAACAGAGGTTATTCATGTGGAAGAGAGCTCGGTGAAT 378
QY 366 GACCACTACATCTTTTACTCCAAAGACAGCACATGSGGGGCTG---CTCCACATGGGA 422
Db 377 GAGCACTACATTTCTACTCGAGAGCGGACAAATGGGACCTGCTCATTCGGGATGGGA 318
QY 423 AAGCTGTGGTAGGAATTCATACCAACCGGAGGCGCTCGAAGAAATTAAGAAATTC 482
Db 317 AAGCTCATGGGGAGAGACTCTGCTGAAATCCAGAGGCCATGGAAGAAATTAAGAAATTC 258
QY 483 GTGCGAGCGCAAGGAGCTCTCGGAGGAGGACATTTTCAGCGCCCTGCGAGAGGAGCTGC 542
Db 257 ATAAAGCGCATGAATCTCCGACTGGAACATGTTTGTGCCAGAGATCGGAGATAATGT 198
QY 543 GTTCCGAACACTAGGAGAGC-CCCGGGCTCTGACCTCCAGAGCGCCACCTACCCAGCA 601
Db 197 GTTGAAGTGAATAGCAGTACCCAGGCTGACAGAGCTGAGCGCCAGCTTCTTCACAC 138
QY 602 CACAGAGCGCGGACCCAGCTGACCTACCTC 632
Db 137 ACCAAGCTGGGACATCCCTTCACACACCTC 107

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Search completed: February 10, 2003, 04:58:27  
Job time : 1927.58 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:02:40 ; Search time 221.524 seconds  
(without alignments)  
8933.518 Million cell updates/sec

Title: US-09-099-823-6

Perfect score: 68

Sequence: 1 AGCTCGGAATTCGAGCTTG.....AGCTCGTGCACCCGGGAAATT 68

Scoring table: IDENTITY\_NOC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.btg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg\_hum.\*

31: em.htg\_inv.\*

32: em.htg\_other.\*

33: em.htg\_mus.\*

34: em.htg\_pln.\*

35: em.htg\_rtd.\*

36: em.htg\_vrt.\*

37: em.htg\_vrt.\*

38: em.sy.\*

39: em.htgo\_hum.\*

40: em.htgo\_mus.\*

41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID       | Description             |
|------------|-------|---------------|--------|-------------|-------------------------|
| 1          | 68    | 100.0         | 68     | AR112296    | AR112296 Sequence       |
| 2          | 68    | 100.0         | 68     | AR123661    | AR123661 Sequence       |
| 3          | 68    | 100.0         | 68     | AR128084    | AR128084 Sequence       |
| 4          | 68    | 100.0         | 68     | AR152175    | AR152175 Sequence       |
| 5          | 68    | 100.0         | 68     | AR195042    | AR195042 Sequence       |
| 6          | 68    | 100.0         | 68     | AR204656    | AR204656 Sequence       |
| 7          | 68    | 100.0         | 68     | AR207544    | AR207544 Sequence       |
| 8          | 68    | 100.0         | 68     | AR210767    | AR210767 Sequence       |
| 9          | 68    | 100.0         | 68     | AR240681    | AR240681 Sequence       |
| 10         | 68    | 100.0         | 68     | BD007433    | BD007433 Reagent a      |
| 11         | 64    | 94.1          | 68     | AR112297    | AR112297 Sequence       |
| 12         | 64    | 94.1          | 68     | AR123662    | AR123662 Sequence       |
| 13         | 64    | 94.1          | 68     | AR128085    | AR128085 Sequence       |
| 14         | 64    | 94.1          | 68     | AR152176    | AR152176 Sequence       |
| 15         | 64    | 94.1          | 68     | AR195043    | AR195043 Sequence       |
| 16         | 64    | 94.1          | 68     | AR204657    | AR204657 Sequence       |
| 17         | 64    | 94.1          | 68     | AR207545    | AR207545 Sequence       |
| 18         | 64    | 94.1          | 68     | AR210768    | AR210768 Sequence       |
| 19         | 64    | 94.1          | 68     | AR240682    | AR240682 Sequence       |
| 20         | 64    | 94.1          | 68     | BD007434    | BD007434 Reagent a      |
| 21         | 54    | 79.4          | 68     | AF244590    | AF244590 Carboxydo      |
| 22         | 54    | 79.4          | 525    | 1 AF244527  | 1 AF244527 Carboxydo    |
| 23         | 54    | 79.4          | 1359   | 10 MSHAPR6B | 10 MSHAPR6B Carboxydo   |
| 24         | 54    | 79.4          | 2174   | 1 AF250348  | 1 AF250348 Carboxydo    |
| 25         | 54    | 79.4          | 2544   | 6 AR175857  | 6 AR175857 Sequence     |
| 26         | 54    | 79.4          | 2806   | 6 AR064707  | 6 AR064707 Sequence     |
| 27         | 54    | 79.4          | 2806   | 6 AR089154  | 6 AR089154 Sequence     |
| 28         | 54    | 79.4          | 3160   | 12 PSVSPORT | 12 PSVSPORT Cloning vec |
| 29         | 54    | 79.4          | 4109   | 12 PSFOT1   | 12 PSFOT1 Cloning vec   |
| 30         | 52.4  | 77.1          | 3327   | 6 AR096545  | 6 AR096545 Sequence     |
| 31         | 52.4  | 77.1          | 3327   | 6 AR140081  | 6 AR140081 Sequence     |
| 32         | 52.4  | 77.1          | 3327   | 6 AR156659  | 6 AR156659 Sequence     |
| 33         | 50.4  | 74.1          | 2208   | 1 BAOFAGEL  | 1 BAOFAGEL Bartonella   |
| 34         | 42    | 61.8          | 3133   | 6 AR138969  | 6 AR138969 Sequence     |
| 35         | 40    | 58.8          | 2288   | 6 AR064706  | 6 AR064706 Sequence     |
| 36         | 40    | 58.8          | 2288   | 6 AR089153  | 6 AR089153 Sequence     |
| 37         | 38.4  | 56.5          | 244    | 6 AX201441  | 6 AX201441 Sequence     |
| 38         | 38.4  | 56.5          | 782    | 6 AX267783  | 6 AX267783 Sequence     |
| 39         | 38.4  | 56.5          | 2060   | 6 AX250222  | 6 AX250222 Sequence     |
| 40         | 37    | 54.4          | 5030   | 6 AR080280  | 6 AR080280 Sequence     |
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| 42         | 31.4  | 46.2          | 4566   | 12 AF177933 | 12 AF177933 Cloning v   |
| 43         | 31.4  | 46.2          | 4733   | 12 XG019585 | 12 XG019585 Cloning vec |
| 44         | 30.2  | 45.6          | 435    | 1 AF244585  | 1 AF244585 Carboxydo    |
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DEFINITION Sequence 17 from patent US 6130043.  
ACCESSION AR112296  
VERSION AR112296.1 GI:14092196  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 68)  
AUTHORS Billings-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,  
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,  
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.  
TITILE Reagents and methods useful for detecting diseases of the prostate

JOURNAL Patent: US 6130043-A 17 10-OCT-2000;

FEATURES Location/Qualifiers

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source /organism="unknown"

BASE COUNT 13 a 20 c 21 g 14 t

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Best Local Similarity 100.0%; Pred. No. 5e-12;

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DB 1 AGCTCGGAATTCGGAGCTTGGATCCTCTAGACGGCGCGCGAGCTAGTGGAGCTCTGCGACC 60

QY 61 CGGGAATT 68

DB 61 CGGGAATT 68

RESULT 2

LOCUS ARL23661

DEFINITION Sequence 11 from patent US 6171787.

ACCESSION ARL23661

VERSION ARL23661.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 68)

AUTHORS Wiley,S.R.

TITLE Member of the TNF family useful for treatment and diagnosis of

disease

JOURNAL Patent: US 6171787-A 11 09-JAN-2001;

FEATURES Location/Qualifiers

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source /organism="unknown"

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LOCUS ARL28084

DEFINITION Sequence 5 from patent US 6183952.

ACCESSION ARL28084

VERSION ARL28084.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 68)

AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,

Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,

Roberts-Rapp,L., Russell,J.C. and Stroupe,S.D.

TITLE Reagents and methods useful for detecting diseases of the breast

JOURNAL Patent: US 6183952-A 5 06-FEB-2001;

FEATURES Location/Qualifiers

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source /organism="unknown"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

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RESULT 4

LOCUS ARL52175

DEFINITION Sequence 9 from patent US 6232456.

ACCESSION ARL52175

VERSION ARL52175.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 68)

AUTHORS Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E., Klass,M.R.,

Russell,J.C., Stewart,K.D. and Stroupe,S.D.

TITLE Serine protease reagents and methods useful for detecting and

treatment diseases of the prostate

JOURNAL Patent: US 6232456-A 9 15-MAY-2001;

FEATURES Location/Qualifiers

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BASE COUNT 13 a 20 c 21 g 14 t

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Best Local Similarity

Matches

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DB

QY

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LOCUS ARL95042

DEFINITION Sequence 5 from patent US 6350583.

ACCESSION ARL95042

VERSION ARL95042.1

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 68)

AUTHORS Cohen,M., Colpitts,T.L., Friedman,P.N., Granados,E.N., Klass,M.R.,

Russell,J.C. and Stroupe,S.D.

TITLE Reagents and methods useful for detecting diseases of the prostate

JOURNAL Patent: US 6350583-A 5 26-FEB-2002;

FEATURES Location/Qualifiers

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source /organism="unknown"

BASE COUNT 13 a 20 c 21 g 14 t

ORIGIN

Query Match

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DB

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DB

Best Local Similarity 100.0%; Pred. No. 5e-12; Mismatches 0; Indels 0; Gaps 0;  
Matches 68; Conservative 0;

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DEFINITION Sequence 19 from patent US 6368792.  
ACCESSION AR204656  
VERSION AR204656.1 GI:21502038  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 68)  
AUTHORS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Hayden, M., Klass, M.R., Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.  
TITLE Reagents and methods useful for detecting diseases of the gastrointestinal tract  
JOURNAL Patent: US 6368792-A 19 09-APR-2002;  
FEATURES Location/Qualifiers  
source 1..68  
BASE COUNT 13 a 20 c 21 g 14 t  
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QY 61 CGGGAATT 68  
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LOCUS AR207544 68 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 3 from patent US 6379671.  
ACCESSION AR207544  
VERSION AR207544.1 GI:21507325  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 68)  
AUTHORS Colpitts, T.L.  
TITLE Reagents and methods useful for detecting diseases of the breast  
JOURNAL Patent: US 6379671-A 3 30-APR-2002;  
FEATURES Location/Qualifiers  
source 1..68  
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DEFINITION Sequence 11 from patent US 6391543.  
ACCESSION AR210767  
VERSION AR210767.1 GI:21513583  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 68)  
AUTHORS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.  
TITLE Reagents and methods useful for detecting diseases of the prostate  
JOURNAL Patent: US 6391543-A 11 21-MAY-2002;  
FEATURES Location/Qualifiers  
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BASE COUNT 13 a 20 c 21 g 14 t  
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Best Local Similarity 100.0%; Pred. No. 5e-12; Mismatches 0; Indels 0; Gaps 0;  
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ACCESSION AX240681  
VERSION AX240681.1 GI:15797664  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 68)  
AUTHORS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.  
TITLE Reagents and methods useful for detecting diseases of the breast  
JOURNAL Patent: WO 0165262-A 7 07-SEP-2001;  
FEATURES Location/Qualifiers  
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RESULT 10
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DEFINITION Reagent and method useful in detecting mammary diseases.
ACCESSION BD007433
VERSION BD007433.1 GI:18635804
KEYWORDS JP 2001503980-A/6.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 68)
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Russell,J.C. and Stroupe,S.D.
TITLE Reagent and method useful in detecting mammary diseases
JOURNAL Patent: JP 2001503980-A 6 27-MAR-2001;
ABBOTT LABORATORIES

COMMENT OS Unidentified
PN JP 2001503980-A/6
PD 27-MAR-2001
PE 31-OCT-1997 JP 1998520795
PF 31-OCT-1996 US 08/742067
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACY L COLPITTS, PI
POLA N FRIEDMAN,
PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES, PI MICHAEL
R KLAAS,
PI JOHN D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL, PI
STEVEN D STROUPE
PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P35/00,C07K14/47,
PC C07K16/30,
PC C12N5/10,C12P21/02,C12P21/02,C12N15/00,C12N5/00,PC
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Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGGGAATT 68
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RESULT 11
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DEFINITION Sequence 18 from patent US 6130043.
ACCESSION AR112297
VERSION AR112297.1 GI:14092197
KEYWORDS
SOURCE Unknown.

REFERENCE 1 (bases 1 to 68)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 68)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,
Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 18 10-OCT-2000;
FEATURES
SOURCE 1..68
LOCATION/Qualifiers
BASE COUNT 15 a 20 c 19 g 14 t
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QY 65 AATT 68
Db 8 AATT 5

RESULT 12
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DEFINITION Sequence 12 from patent US 6171787.
ACCESSION AR123662
VERSION AR123662.1 GI:14109023
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 68)
AUTHORS Wiley,S.R.
TITLE Member of the TNF family useful for treatment and diagnosis of
disease
JOURNAL Patent: US 6171787-A 12 09-JAN-2001;
FEATURES
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LOCATION/Qualifiers
BASE COUNT 15 a 20 c 19 g 14 t
ORIGIN

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Db 8 AATT 5

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DEFINITION Sequence 6 from patent US 6183952.
ACCESSION AR128085
VERSION AR128085.1 GI:14115747
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 68)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N.,

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Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,  
Roberts-Rapp, L., Russell, J.C. and Stroupe, S.D.

Reagents and methods useful for detecting diseases of the breast

Patent: US 6183952-A 6 06-FEB-2001;

Location/Qualifiers  
source

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Best Local Similarity 100.0%; Pred. No. 1e-10;

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 26                 | 64 | 94.1  | 68 | 19 | AAV62336 |
| 27                 | 64 | 94.1  | 68 | 20 | AAV78711 |
| 28                 | 64 | 94.1  | 68 | 20 | AAV72659 |
| 29                 | 64 | 94.1  | 68 | 20 | AAK37322 |
| 30                 | 64 | 94.1  | 68 | 20 | AAK07459 |
| 31                 | 64 | 94.1  | 68 | 20 | AAV71183 |
| 32                 | 64 | 94.1  | 68 | 21 | AAV64848 |
| 33                 | 64 | 94.1  | 68 | 21 | AAC64930 |
| 34                 | 64 | 94.1  | 68 | 21 | AAA94072 |
| 35                 | 64 | 94.1  | 68 | 21 | AAA37697 |
| 36                 | 64 | 94.1  | 68 | 22 | AAD18676 |
| 37                 | 64 | 94.1  | 68 | 22 | AAD13639 |
| 38                 | 64 | 94.1  | 68 | 22 | AAD14844 |
| 39                 | 64 | 94.1  | 68 | 22 | AAS07157 |
| 40                 | 64 | 94.1  | 68 | 24 | AAL40055 |
| 41                 | 64 | 94.1  | 68 | 24 | AAD35798 |
| 42                 | 64 | 94.1  | 68 | 24 | AAD35927 |
| 43                 | 64 | 94.1  | 68 | 24 | AAD34485 |
| 44                 | 64 | 94.1  | 68 | 24 | AAD34492 |
| 45                 | 64 | 94.1  | 68 | 24 | AAD34492 |
| Human prostate-rel |    |       |    |    |          |
| Human TGF-beta sup |    |       |    |    |          |
| Linker used to iso |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Breast tissue libr |    |       |    |    |          |
| Oligonucleotide us |    |       |    |    |          |
| B5203-related DNA  |    |       |    |    |          |
| Human CS193-relat  |    |       |    |    |          |
| P5215-related DNA  |    |       |    |    |          |
| Human P5190-relat  |    |       |    |    |          |
| Human P5190-relat  |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Nucleotide sequenc |    |       |    |    |          |
| Nucleotide sequenc |    |       |    |    |          |
| Plasmid pINCY DNA  |    |       |    |    |          |
| PINC1 primer 2, S  |    |       |    |    |          |
| Human B5274 protei |    |       |    |    |          |
| Human breast-speci |    |       |    |    |          |
| Synthetic pINCY po |    |       |    |    |          |
| Nucleotide sequenc |    |       |    |    |          |
| Synthetic polylink |    |       |    |    |          |
| Human prostate-rel |    |       |    |    |          |
| Human TGF-beta sup |    |       |    |    |          |
| Linker used to iso |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Synthetic DNA frag |    |       |    |    |          |
| Breast tissue libr |    |       |    |    |          |
| B5203-related DNA  |    |       |    |    |          |
|                    |    |       |    |    |          |

## ALIGNMENTS

RESULT 1  
AAV63517  
ID AAV63517 standard; CDNA: 68 BP.

XX  
-AC-  
AAV63517:XX  
DT 28-JAN-1999 (first entry)

XX Nucleotide sequence of the specification.

EST sequence; CS141; gastrointestinal tract; cancer; Barret's esophagus;  
gastric ulcer; gastritis; leiomyoma; polyps; Crohn's disease;  
ulcerative colitis; pancreatitis; SS.

AA  
OS  
Synthetic.

03  
05  
05

XX  
PN W09844133-A1.

XX 08-007-1998

XX  
PF 31-MAR-1998: 98WQ-US06337.

XX 31-MAR-1997. 07PG-0828189

XX  
XX  
XX

XX Billing-Medel Pa, Cohen M, Colpitts Tt, Friedman PN;  
PI Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR;  
PI Kratochvil JD, Roberts-rapp L, Russell JC, Stroupe SD;  
XX WPI; 1998-568280/48.



XX PT New gastrointestinal tract specific polynucleotides, CS141 - used to  
 PT develop products for the diagnosis and treatment of e.g. cancers,  
 PT gastric ulcer, gastritis, Crohn's disease, ulcerative colitis or  
 PT pancreatitis  
 XX  
 PS Disclosure; Page 93; 116pp; English.  
 XX  
 CC The present sequence appears in the specification, which describes  
 CC a set of contiguous and partially overlapping EST sequences designated  
 CC CS141. The sequences are isolated from a cDNA library made from  
 CC gastrointestinal tract tumour and normal tissues. The polypeptides are  
 CC useful as a marker for gastrointestinal tract disorders. The CS141 gene is  
 CC and products can be used in detecting, diagnosing, staging, monitoring,  
 CC prognosticating, preventing, or determining the predisposition to  
 CC diseases and conditions of the gastrointestinal tract, such as  
 CC gastrointestinal tract cancers, Barrett's esophagus, gastric ulcer,  
 CC gastritis, leiomyoma, polyps, Crohn's disease, ulcerative colitis,  
 CC pancreatitis.  
 XX  
 SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 19; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATCCGAGTTCGGATCTCTAGAGCGCGCGCGGACTAGTGTCTGTGACC 60  
 DB 1 AGCTCGGAATCCGAGTTCGGATCTCTAGAGCGCGCGCGGACTAGTGTCTGTGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

RESULT 2  
 AAV63529  
 ID AAV63529 standard; cDNA; 68 BP.

XX AC AAV63529;  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE Nucleotide sequence of the specification.  
 KW EST sequence; CS110; gastrointestinal tract; cancer; adenocarcinoma;  
 KW lymphoma; ss.  
 OS Homo sapiens.  
 XX  
 PN WO9844160-AL.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 31-MAR-1998; 98WO-US06338.  
 XX  
 PR 31-MAR-1997; 97US-0829755.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;  
 PI Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR;  
 PI Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1998-557139/47.  
 XX  
 CC New CS110 polypeptide(s) - useful for detecting gastrointestinal  
 PT tract diseases, e.g. gastrointestinal tract cancers and to produce  
 PT antibodies  
 XX  
 PS Disclosure; Page 91; 116pp; English.  
 XX  
 CC The present sequence appears in the specification, which describes

CC a set of contiguous and partially overlapping EST sequences designated  
 CC CS110. The sequences are isolated from a cDNA library made from  
 CC gastrointestinal tract tumour and normal tissues. The polypeptides are  
 CC useful diagnostically to detect CS110 antigen/anti-CS110 antibody in  
 CC samples, e.g. to detect diseases and conditions of the gastrointestinal  
 CC tract, especially cancers, e.g. adenocarcinoma and lymphoma.  
 XX  
 SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 19; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATCCGAGTTCGGATCTCTAGAGCGCGCGCGGACTAGTGTCTGTGACC 60  
 DB 1 AGCTCGGAATCCGAGTTCGGATCTCTAGAGCGCGCGCGGACTAGTGTCTGTGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

RESULT 3  
 AAV62335  
 ID AAV62335 standard; DNA; 68 BP.

XX AC AAV62335;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Plasmid pINCY DNA fragment #1.  
 XX  
 KW Gastrointestinal tract; GI tract; cancer; disease; detection; CS198;  
 KW human; predisposition; treatment; Barrett's oesophagus; gastric ulcer;  
 KW gastritis; leiomyoma; polyps; Crohn's disease; ulcerative colitis;  
 KW pancreatitis; ss.  
 OS Homo sapiens.  
 XX  
 PN WO9844159-AL.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 30-MAR-1998; 98WO-US06251.  
 XX  
 PR 31-MAR-1997; 97US-0828855.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;  
 PI Gordon J, Granados EN, Hayden M, Hodges SC, Klass MR;  
 PI Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1998-542714/46.  
 XX  
 CC New gastrointestinal polynucleotides, CS198, and their detection -  
 PT used for developing products for the diagnosis and treatment of  
 PT gastrointestinal disorders, e.g. cancers, gastric ulcer or gastritis  
 PT  
 PS Disclosure; Page 98; 127pp; English.  
 XX  
 CC This sequence is a fragment of the plasmid pINCY which is used in a  
 CC method to detect in a method to detect the presence of a target human  
 CC CS198 polynucleotide in a test sample. The CS198 gene is useful as a  
 CC marker for gastrointestinal (GI) tract disorders. The methods and  
 CC products can be used in detecting, diagnosing, staging, monitoring,  
 CC prognosticating, preventing or treating, or determining the  
 CC predisposition to diseases and conditions of the GI tract, such as GI  
 CC tract cancer, Barrett's oesophagus, gastric ulcer, gastritis, leiomyoma,  
 CC polyps, Crohn's disease, ulcerative colitis, and pancreatitis.  
 XX  
 SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 19; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGAGCTAGTGTCTGTGACG 60  
 DB 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGAGCTAGTGTCTGTGACG 60

OY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

RESULT 4  
 AAX78710  
 ID AAX78710 standard; DNA: 68 BP.  
 XX  
 AC AAX78710;  
 DT 03-SEP-1999 (first entry)  
 XX  
 DE pINCY primer 1.  
 XX  
 KW Pancreatic disease; PA153; human; cytostatic; detection; antigen;  
 KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;  
 KW gene therapy; pINCY; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9931274-A2.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 11-DEC-1998; 98WO-US26441.  
 XX  
 PR 15-DEC-1997; 97US-0990568.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PM;  
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1999-405041/34.  
 XX  
 PT PA153 cDNA transcribed from pancreatic tissue  
 XX  
 PS Disclosure; Page 119; 123pp; English.  
 XX  
 CC This invention describes novel contiguous and partially overlapping  
 CC cDNA sequences and their encoded polypeptides, designated PA153,  
 CC transcribed from human pancreatic tissue and which have cytostatic  
 CC activity. The PA153 polynucleotides, proteins and antibodies are all  
 CC useful in methods of detection. Detection of PA153 polynucleotide,  
 CC antigen or anti-PA153 antibodies in a sample is indicative of  
 CC pancreatic disease. PA153 antibodies (antagonists) can also be used in  
 CC vivo for therapeutic use, e.g. treatment of pancreatic disease, tumours  
 CC or metastases. Antisense PA153 polynucleotides can be used in gene  
 CC therapy of pancreatic diseases. This sequence represents a pINCY primer  
 CC used in the method of the invention.  
 XX  
 SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 20; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGAGCTAGTGTCTGTGACG 60  
 DB 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGAGCTAGTGTCTGTGACG 60

OY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

DB 61 CGGGAATT 68

RESULT 5  
 AAV72368  
 ID AAV72368 standard; DNA: 68 BP.  
 XX  
 AC AAV72368;  
 DT 29-JUL-1999 (first entry)  
 XX  
 DE Human BS274 protein primer 1.  
 XX  
 KW Human; breast tissue; BS274; detection; disease; marker; antitumour;  
 KW breast cancer; metastases; atypical hyperplasia; fibroadenoma; cyst;  
 KW diagnosis; therapy; cytotoxin; immunoscreen; immunoscreen;  
 KW chromosomal anomaly; immunisation; antisense; triplex; ribozyme;  
 KW primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9925850-A1.  
 XX  
 PD 27-MAY-1999.  
 XX  
 PF 17-NOV-1998; 98WO-US24562.  
 XX  
 PR 17-NOV-1997; 97US-0971772.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PM;  
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI; 1999-347484/29.  
 XX  
 PT New BS274 nucleic acid as a marker for breast disease  
 XX  
 PS Disclosure; Page 99; 105pp; English.  
 XX  
 CC This invention describes novel human BS274 protein clones which can be  
 CC used as markers for breast cancer and have antitumour activity. BS274  
 CC can also be used as a marker of cancer and its metastases, atypical  
 CC hyperplasia, fibroadenoma and cysts, so detection/quantification of  
 CC BS274 encoded polypeptides and BS274-specific antibodies are used  
 CC for diagnosis, staging, monitoring, prognosis, in vivo imaging of, and  
 CC determining predisposition to these diseases. Antibodies are useful as  
 CC therapeutic antagonists (optionally coupled to a cytotoxin), as  
 CC immunoscreening reagents and in competitive drug screens. BS274 nucleic acid  
 CC and its fragments, are used as probes and primers (in diagnostic assays,  
 CC for quantifying gene expression, for detecting chromosomal anomalies and  
 CC to isolate related sequences), for genetic immunization, as a source of  
 CC recombinant production of BS274 polypeptides. BS274 polypeptides are  
 CC used as immunoscreening reagents, for generating antibodies, and for  
 CC for specific binding agents (i.e. antagonists and inhibitors, potentially  
 CC useful as therapeutic agents) and for rational drug design.  
 XX  
 SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 20; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGAGCTAGTGTCTGTGACG 60  
 DB 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGAGCTAGTGTCTGTGACG 60

OY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

RESULT 6  
 AAX37321  
 ID AAX37321 standard; DNA; 68 BP.  
 XX AC AAX37321;  
 XX DT 05-JUL-1999 (first entry)  
 XX DE Human breast-specific BS200 DNA primer 1.  
 XX KW Breast; cancer; BS200; EST; expressed sequence tag; human; detection;  
 XX KW diagnosis; prevention; treatment; disease predisposition; primer; ss.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN W09902714-A1.  
 XX PD 21-JAN-1999.  
 XX PF 07-JUL-1998; 98WO-US13908.  
 XX PR 07-JUL-1997; 97US-0889127.  
 XX PS (ABBO ) ABBOTT LAB.  
 XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;  
 XX PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
 XX PI Russell JC, Stroupe SD, Yu H;  
 XX DR WPI; 1999-120915/10.  
 XX PT New breast specific gene BS200 - used to develop products for  
 XX PT detecting, diagnosing, staging, preventing or treating diseases or  
 XX PT conditions of the breast, e.g. breast cancer  
 XX PS Disclosure; Page 114; 124pp; English.  
 XX CC This invention describes a novel human breast-specific protein BS200.  
 XX CC This protein and its encoding nucleic acids are useful for detecting,  
 XX CC diagnosing, staging, monitoring, prognosticating, preventing or treating,  
 XX CC or determining predisposition to diseases or conditions of the breast,  
 XX CC such as breast cancer.  
 XX SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 Query Match 100.0%; Score 68; DB 20; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGTGGATCTCTAGAGCGGCGCGGACTAGTGTGCTGCGACC 60  
 DB 1 AGCTCGGAATTCGAGTGGATCTCTAGAGCGGCGGCGGACTAGTGTGCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68  
 RESULT 7  
 AAX07458  
 ID AAX07458 standard; cDNA; 68 BP.  
 XX AC AAX07458;  
 XX DT 08-JUN-1999 (first entry)  
 XX DE Synthetic pINCY polylinker fragment.  
 XX KW BS124; breast; cancer; detection; diagnosis; prevention; treatment;  
 XX KW pINCY; polylinker; ss.  
 Query Match 100.0%; Score 68; DB 20; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGTGGATCTCTAGAGCGGCGGCGGACTAGTGTGCTGCGACC 60  
 DB 1 AGCTCGGAATTCGAGTGGATCTCTAGAGCGGCGGCGGACTAGTGTGCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

XX OS Synthetic.  
 XX PN W09859049-A1.  
 XX PD 30-DEC-1998.  
 XX PF 19-JUN-1998; 98WO-US12862.  
 XX PR 20-JUN-1997; 97US-0879354.  
 XX PA (ABBO ) ABBOTT LAB.  
 XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;  
 XX PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
 XX PI Russell JC, Scheffel CP, Stroupe SD, Yu H;  
 XX DR WPI; 1999-105623/09.  
 XX PT New isolated BS124 polynucleotides and polypeptides - used for  
 XX PT detecting, diagnosing, preventing or treating diseases or conditions  
 XX PT of the breast, such as breast cancer  
 XX PS Disclosure; Page 95; 125pp; English.  
 XX CC The sequence is that of a pINCY polylinker fragment which was  
 XX CC used in the construction of an expression vector for a BS124-specific  
 XX CC EST clone. Such a clone is useful for detecting, diagnosing, staging,  
 XX CC preventing or treating, or determining predisposition to diseases or  
 XX CC conditions of the breast, such as breast cancer.  
 XX SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 Query Match 100.0%; Score 68; DB 20; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGTGGATCTCTAGAGCGGCGGCGGACTAGTGTGCTGCGACC 60  
 DB 1 AGCTCGGAATTCGAGTGGATCTCTAGAGCGGCGGCGGACTAGTGTGCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68  
 RESULT 8  
 AAV71182  
 ID AAV71182 standard; DNA; 68 BP.  
 XX AC AAV71182;  
 XX DT 12-FEB-1999 (first entry)  
 XX DE Nucleotide sequence of the specification.  
 XX KW PS108 gene; prostate disease; benign prostatic hyperplasia; BPH;  
 XX KW prostatitis; prostatic intraepithelial neoplasia; PIN; cancer;  
 XX KW drug screening; gene therapy; ss.  
 XX OS Homo sapiens.  
 XX PN W09850567-A1.  
 XX PD 12-NOV-1998.  
 XX PF 01-MAY-1998; 98WO-US08930.  
 XX PR 02-MAY-1997; 97US-0850713.  
 XX PA (ABBO ) ABBOTT LAB.  
 XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;

PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD;  
 DR WPI; 1999-034731/03.  
 XX New isolated prostate-specific polynucleotides - used to develop  
 PT products for the diagnosis and treatment of prostate diseases, e.g.  
 PT benign hyperplasia, prostatic or prostate cancer  
 XX Disclosure; Page 96; 122pp; English.  
 CC The present sequence appears in the specification, which describes  
 CC a method for detecting the presence of a target PS108 polynucleotide  
 CC in a test sample. The method comprises contacting the test sample  
 CC with at least 1 PS108-specific polynucleotide or complement, and  
 CC detecting the presence of the target PS108 polynucleotide. The  
 CC products can be used for detecting, diagnosing, staging, monitoring,  
 CC prognosticating, in vivo imaging, preventing or treating, or  
 CC determining predisposition to diseases or conditions of the  
 CC prostate such as benign prostatic hyperplasia (BPH), prostatitis,  
 CC prostatic intraepithelial neoplasia (PIN) and cancer. In particular  
 CC the products can be used in drug screening and gene therapy.  
 XX Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 SQ Query Match 100.0%; Score 68; DB 20; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGGCGGACTAGTGTCTGCGACC 60  
 DB 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGGCGGACTAGTGTCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68  
 RESULT 9  
 AA64847  
 ID AA64847 standard; DNA; 68 BP.  
 AC AA64847;  
 DT 20-JUN-2001 (first entry)  
 DE Synthetic polylinker sequence # 1 used in plasmid pINCY construction.  
 KW Breast cancer; breast disease detection; mamaglobin; pINCY;  
 KW uteroglobin; BU101; endometrial; cytostatic; ss.  
 OS Synthetic.  
 PN WC200035950-A2.  
 XX 22-JUN-2000.  
 XX 20-DEC-1999; 99WO-US30489.  
 XX 18-DEC-1998; 98US-0215818.  
 XX (ABBO) ABBOTT LAB.  
 PI Colpitts TL, Russell JE;  
 DR WPI; 2000-442366/38.  
 XX Multimeric polypeptide antigen and antibody specific to the antigen are  
 PT useful for diagnosing, detecting and treating breast cancer.  
 XX Disclosure; Page 123; 124pp; English.  
 PS Mamaglobin and BU101 are members of the uteroglobin protein family.

CC The coding sequences for human mamaglobin and BU101 have been isolated  
 CC (see AA64845 and AA64846). The present invention relates to a  
 CC multimeric polypeptide antigen, which comprises of the mamaglobin and  
 CC BU101 proteins. The presence of multimeric polypeptide antigen in a test  
 CC sample can be used as the basis for a test to diagnose breast disease  
 CC e.g. breast cancer, in a patient. The detection can be carried out using  
 CC antibodies specific for the multimeric polypeptide antigen. The present  
 CC sequence is a synthetic polylinker used in the construction of plasmid  
 CC pINCY. pINCY was used to clone the coding sequences of mamaglobin and  
 CC BU101.  
 XX Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 SQ Query Match 100.0%; Score 68; DB 21; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGGCGGACTAGTGTCTGCGACC 60  
 DB 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGGCGGACTAGTGTCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68  
 RESULT 10  
 AAC64929  
 ID AAC64929 standard; DNA; 68 BP.  
 AC AAC64929;  
 DT 07-FEB-2001 (first entry)  
 DE Human prostate-related PS108 vector fragment SEQ ID NO: 17.  
 KW Human; prostate cancer; PS108; antibody; tumour; metastasis; vector; ds.  
 OS Synthetic.  
 PN US6130043-A.  
 PD 10-OCT-2000.  
 PF 01-MAY-1998; 98US-0071710.  
 PR 02-MAY-1997; 97US-0850713.  
 XX (ABBO) ABBOTT LAB.  
 PI Cohen M, Colpitts TL, Friedman PN, Gordon J, Granados EN;  
 PI Billing-Wedel PA, Klass MR, Roberts-Rapp L, Stroupe SD, Fu H;  
 PI Kratochvil JD, Russell JC, Hodges SC;  
 XX WPI; 2000-655655/63.  
 XX Methods for detecting target prostate-specific polynucleotides or  
 XX diseases of the prostate (e.g. prostate cancer), comprising detecting  
 XX the presence of any of PS108 nucleic acid sequences in a test sample -  
 XX Disclosure; Column 79-80; 55pp; English.  
 CC The present invention is related to a number of partial coding and  
 CC protein sequences for the human prostate tissue protein PS108. These  
 CC sequences can be used in the diagnosis and prognosis of prostate  
 CC diseases, particularly prostate cancer. They can also be used to produce  
 CC antibodies which can be used in treatment. The present sequence is one  
 CC of the PS108 partial coding sequences.  
 XX Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 SQ Query Match 100.0%; Score 68; DB 21; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;

Matches: 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGAGTACTAGTCTGTCGACC 60  
 |||||  
 Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGAGTACTAGTCTGTCGACC 60  
 |||||

QY 61 CGGGAATT 68  
 |||||

Db 61 CGGGAATT 68

RESULT 11

AAA94071  
 ID AAA94071 standard; DNA; 68 BP.  
 AC AAA94071;  
 XX  
 DT 30-JAN-2001 (first entry)  
 XX  
 DE Human TGF-beta superfamily protein PCIGF vector oligonucleotide #1.  
 XX  
 KW Human; TGF-beta superfamily; prostate cancer-induced growth factor;  
 KW PCIGF; prostate disease; prostate cancer; benign prostatic hyperplasia;  
 KW prostatitis; prostatic intraepithelial neoplasia; vector production; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200056352-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US07945.  
 XX  
 PR 25-MAR-1999; 99US-0276600.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Gordon J, Granados EN;  
 PI Russell JC, Stroupe SD;  
 DR WPI; 2000-628218/60.  
 XX  
 PT Novel prostate cancer induced growth factor derived polynucleotide  
 PT useful for detecting, diagnosing, prognosing, preventing or treating  
 PT conditions of the prostate, especially prostate cancer.  
 XX  
 PS Disclosure; Page 114; 117pp; English.

The present sequence is an oligonucleotide used during the production of  
 an expression vector containing the coding sequence for the human  
 prostate cancer-induced growth factor (PCIGF). The protein is a member of  
 the TGF-beta superfamily. The 3' part of the gene has been shown to be  
 upregulated in prostate cancer, and thus can be used in the diagnosis of  
 the disease. It is also useful for the identification of antigens to  
 the PCIGF protein which can be used to treat cancer. In addition, benign  
 prostatic hyperplasia, prostatitis and prostatic intraepithelial  
 neoplasia can be detected using the gene and protein.

Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 21; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGAGTACTAGTCTGTCGACC 60  
 |||||  
 Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGAGTACTAGTCTGTCGACC 60  
 |||||

QY 61 CGGGAATT 68  
 |||||

Db 61 CGGGAATT 68

RESULT 12

AAA37696  
 ID AAA37696 standard; DNA; 68 BP.  
 XX  
 AC AAA37696;  
 XX  
 DT 28-OCT-2000 (first entry)  
 XX  
 DE Linker used to isolate BS325 coding sequence clones.  
 XX  
 KW BS325; diagnosis; breast disease; breast cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200043421-A1.  
 XX  
 PD 27-JUL-2000.  
 XX  
 PF 21-JAN-2000; 2000WO-US01556.  
 XX  
 PR 21-JAN-1999; 99US-0234717.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PM, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;  
 PI Stroupe SD;  
 DR WPI; 2000-505832/45.  
 XX  
 PT Novel methods for the detecting the presence of target BS325  
 PT polypeptides and polynucleotides, used for identifying and monitoring  
 PT diseases of the breast  
 XX  
 PS Disclosure; Page 116; 122pp; English.

This sequence was used to isolate BS325 coding sequence clones. The  
 invention relates to a method of detecting the presence of a target BS325  
 polynucleotide in a test sample comprises: (a) contacting the test sample  
 with at least one BS325-specific polynucleotide or complement thereof;  
 CC and (b) detecting the presence of BS325 polynucleotides from the test  
 sample. The method is used to enable the identification of certain  
 markers as indicative of a breast tissue disease or condition. The  
 methods can be used for detecting, diagnosing, staging, monitoring,  
 CC prognosticating, in vivo imaging, preventing, or treating conditions  
 CC associated with BS325, especially breast cancer. The BS325 polypeptides  
 CC can be used to raise antibodies, and to identify agonists and  
 CC antagonists. The BS325 polynucleotides are used as a source of probes  
 CC and primers. The invention provides an alternative, non-surgical  
 CC diagnostic methods which are capable of detecting early stage breast  
 CC disease, such as cancer.

Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;

Query Match 100.0%; Score 68; DB 21; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGAGTACTAGTCTGTCGACC 60  
 |||||  
 Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGAGTACTAGTCTGTCGACC 60  
 |||||

QY 61 CGGGAATT 68  
 |||||

Db 61 CGGGAATT 68

RESULT 13

AAD18675  
 ID AAD18675 standard; DNA; 68 BP.  
 XX  
 AC AAD18675;  
 XX

DT 18-DEC-2001 (first entry)  
 XX Synthetic DNA fragment #1 used to construct plasmid pINCY.  
 XX Human; BSI06 protein; breast cancer; metastasis; gene therapy;  
 KW tumour; expressed sequence tag; EST; ds.  
 XX Synthetic.  
 OS  
 XX WO200165262-A2.  
 XX  
 XX PD 07-SEP-2001.  
 XX  
 XX PD 28-FEB-2001; 2001WO-US06516.  
 XX PD 29-FEB-2000; 2000US-0516444.  
 XX PD (ABBO) ABBOTT LAB.  
 XX  
 XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;  
 PI Russell JC, Stroupe SD;  
 XX WPI; 2001-596773/67.  
 XX  
 XX A gene or its fragment which codes for a BSI06 polypeptide, useful for  
 PT the detection of a breast disease such as breast cancer -  
 PT  
 XX Disclosure; Page 150; 158pp; English.  
 PS  
 XX The invention relates to human BSI06-specific polypeptides and  
 CC polynucleotides. The BSI06 polypeptides and antibodies are useful  
 CC for detecting, diagnosing, staging, monitoring, prognosticating,  
 CC preventing, treating or determining the predisposition of an  
 CC individual to diseases and conditions of the breast such as breast  
 CC cancer. They are also useful in the treatment of tumours or  
 CC metastases. Polynucleotides of the invention are useful in drug  
 CC screening and gene therapy. The present sequence is a synthetic  
 CC DNA fragment used to construct pINCY plasmid which comprises  
 CC human BSI06 gene cDNA, expressed sequence tag (EST) clone 1652885.  
 XX  
 XX Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 68; DB 22; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGCCTGCGACC 60  
 Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGCCTGCGACC 60  
 QY 61 CGGGAATT 68  
 Db 61 CGGGAATT 68  
 RESULT 14  
 AAD13638  
 ID AAD13638 standard; DNA; 68 BP.  
 XX  
 XX AAD13638;  
 XX  
 XX 06-NOV-2001 (first entry)  
 XX  
 XX Synthetic DNA fragment #1 for generating pINCY plasmid.  
 XX  
 XX CS 198; gastrointestinal tract disease; GI tract; cancer; gastric ulcer;  
 KW gastritis; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW Barrett's oesophagus; gene therapy; drug screening; pINCY plasmid; ds.  
 XX Synthetic.  
 OS  
 XX US2001010904-A1.  
 PN

XX 02-AUG-2001.  
 PD  
 XX 30-MAR-1998; 98US-0050516.  
 PF  
 XX 31-MAR-1997; 97US-0828855.  
 PR  
 XX (BILL) BILLING-MEDEL P A.  
 PA (COHE) COHEN M.  
 PA (COLP) COLPITTS T L.  
 PA (FRIE) FRIEDMAN P N.  
 PA (GORD) GORDON J.  
 PA (GRAN) GRANADOS E N.  
 PA (HAYD) HAYDEN M.  
 PA (HODG) HODGES S C.  
 PA (KLAS) KLASS M R.  
 PA (KRAT) KRATOCHVIL J D.  
 PA (ROBE) ROBERTS-RAPP L.  
 PA (RUSSE) RUSSELL J C.  
 PA (STRO) STROUPE S D.  
 XX  
 XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hayden M, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-Rapp L, Russell JC, Stroupe SD;  
 PI  
 XX WPI; 2001-496163/54.  
 XX  
 XX Detecting the presence of target CS 198 polynucleotide, useful for  
 PT detecting or diagnosing diseases of the gastrointestinal tract,  
 PT comprises contacting test sample with at least one CS 198-specific  
 PT polynucleotide -  
 XX  
 XX Disclosure; Page 47; 68pp; English.  
 XX  
 XX The invention relates to a method of detecting the presence of a target  
 CC CS 198 polynucleotide comprising contacting the test sample with at  
 CC least one CS 198-specific polynucleotide. The method is useful for  
 CC detecting diseases of the gastrointestinal (GI) tract organs,  
 CC particularly cancer. The CS 198 polynucleotides, polypeptides and  
 CC antibodies are useful for detecting, diagnosing, staging, monitoring,  
 CC prognosticating, preventing, treating or determining predisposition to  
 CC diseases and conditions of the GI tract such as cancer, gastric ulcer,  
 CC gastritis, Crohn's disease, ulcerative colitis, pancreatitis and  
 CC Barrett's oesophagus. The CS 198 polypeptides are useful as standards  
 CC or reagents in diagnostic immunoassays, as components or as  
 CC target sites for various therapies. Antibodies directed against at  
 CC least one epitope contained within these polypeptides are useful as  
 CC delivery agents for therapeutic agents, in diagnostic tests and for  
 CC screening for conditions or diseases associated with CS 198,  
 CC particularly cancer. Monoclonal antibodies may also be used for the  
 CC generation of chimeric antibodies for therapeutic use. The CS 198  
 CC polynucleotide is also useful in gene therapy and drug screening.  
 CC The method of the invention provides an alternative, non-surgical,  
 CC diagnostic method capable of detecting early stage GI tract disease  
 CC such as cancer. The present sequence is a synthetic DNA fragment  
 CC used for creating pINCY plasmid which is used as an expression vector  
 CC for CS 198 polypeptide.  
 XX  
 XX Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 68; DB 22; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGCCTGCGACC 60  
 Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGCCTGCGACC 60  
 QY 61 CGGGAATT 68  
 Db 61 CGGGAATT 68

RESULT 15  
 AAD14843  
 ID AAD14843 standard; DNA; 68 BP.  
 XX  
 AC AAD14843;  
 XX  
 DT 01-NOV-2001 (first entry)  
 XX  
 DE Synthetic DNA fragment #1, to generate P1NCY plasmid.  
 XX  
 KW PS133; prostate disease; cancer; immunogen; gene therapy; cytostatic;  
 KW P1NCY plasmid; ds.  
 XX  
 OS Synthetic.  
 XX  
 FW US6232456-B1.  
 XX  
 PD 15-MAY-2001.  
 XX  
 PF 06-OCT-1997; 97US-0944483.  
 XX  
 PR 06-OCT-1997; 97US-0944483.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;  
 PI Russell JC, Stewart KD, Stroupe SD;  
 XX  
 DR WPI; 2001-366357/38.  
 XX  
 PT New PS133 polynucleotides, useful for detecting, diagnosing, staging,  
 PT monitoring, prognosing, preventing, treating or determining the  
 PT predisposition of an individual to a prostate disease, e.g. cancer -  
 XX  
 PS Disclosure; Column 73-74; 93pp; English.  
 XX  
 CC The patent discloses PS-133 polynucleotides and polypeptides which  
 CC are indicative of prostate disease. The patent also provides a method  
 CC for detecting PS133 protein in a test sample. The polynucleotides of  
 CC the invention are useful for detecting, diagnosing, staging, monitoring,  
 CC prognosing, preventing, treating or determining the predisposition of  
 CC an individual to prostate diseases such as cancer. PS133-derived  
 CC polynucleotides are used for the detection of normal or altered gene  
 CC expression, in assays for detecting, amplifying or quantifying genes  
 CC or nucleic acids relating to prostate tissue diseases and conditions,  
 CC and to produce probes which can be used in the detection of nucleic  
 CC acids in a sample. PS-133 proteins are used as immunogens for the  
 CC production of antibodies. PS-133 sequences are also used in gene  
 CC therapy. The present sequence is a synthetic DNA fragment which is  
 CC used in the generation of P1NCY plasmid comprising PS133 sequence.  
 CC P1NCY is generated from plasmid pSPORI1.  
 XX  
 SQ Sequence 68 BP; 13 A; 20 C; 21 G; 14 T; 0 other;  
 XX  
 Query Match 100.0%; Score 68; DB 22; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.le-15;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGCCTGCGACC 60  
 Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGCCTGCGACC 60  
 QY 61 CGGGAATT 68  
 Db 61 CGGGAATT 68

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 20:30:25 ; Search time 4.94273 Seconds  
(without alignments)  
4219.129 Million cell updates/sec

Title: US-09-099-823-6

Perfect score: 68

Sequence: 1 AGCTGGGATTCGAGCTTG.....AGCTGCTGACCGGGGATT 68

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapert 1.0

Searched: 441362 seqs, 15339381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgm2\_6/prodata/1/ina/5A.COMB.seq.\*
- 2: /cgm2\_6/prodata/1/ina/5B.COMB.seq.\*
- 3: /cgm2\_6/prodata/1/ina/6A.COMB.seq.\*
- 4: /cgm2\_6/prodata/1/ina/6B.COMB.seq.\*
- 5: /cgm2\_6/prodata/1/ina/PTGUS.COMB.seq.\*
- 6: /cgm2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description       |
|------------|-------|-------|--------|-------|-------------------|
| 1          | 68    | 100.0 | 68     | 2     | US-08-964-725-6   |
| 2          | 68    | 100.0 | 68     | 3     | Sequence 6, Appli |
| 3          | 68    | 100.0 | 68     | 4     | Sequence 17, Appl |
| 4          | 68    | 100.0 | 68     | 4     | Sequence 11, Appl |
| 5          | 68    | 100.0 | 68     | 4     | Sequence 5, Appli |
| 6          | 68    | 100.0 | 68     | 4     | Sequence 9, Appli |
| 7          | 68    | 100.0 | 68     | 4     | Sequence 17, Appl |
| 8          | 68    | 100.0 | 68     | 4     | Sequence 5, Appli |
| 9          | 68    | 100.0 | 68     | 4     | Sequence 19, Appl |
| 10         | 68    | 100.0 | 68     | 4     | Sequence 3, Appli |
| 11         | 68    | 100.0 | 68     | 4     | Sequence 11, Appl |
| 12         | 68    | 100.0 | 68     | 4     | Sequence 2, Appli |
| 13         | 64    | 94.1  | 68     | 3     | US-09-071-710-17  |
| 14         | 64    | 94.1  | 68     | 4     | US-08-883-086-11  |
| 15         | 64    | 94.1  | 68     | 4     | US-08-912-276-5   |
| 16         | 64    | 94.1  | 68     | 4     | US-08-944-483-9   |
| 17         | 64    | 94.1  | 68     | 4     | US-09-525-397-17  |
| 18         | 64    | 94.1  | 68     | 4     | US-09-566-876-5   |
| 19         | 64    | 94.1  | 68     | 4     | US-09-049-698-19  |
| 20         | 64    | 94.1  | 68     | 4     | US-09-215-818-3   |
| 21         | 64    | 94.1  | 68     | 4     | US-09-065-383-11  |
| 22         | 64    | 94.1  | 68     | 4     | US-09-276-600-2   |
| 23         | 64    | 94.1  | 68     | 4     | US-09-964-725-7   |
| 24         | 64    | 94.1  | 68     | 4     | US-09-071-710-18  |
| 25         | 64    | 94.1  | 68     | 4     | US-08-883-086-12  |
| 26         | 64    | 94.1  | 68     | 4     | US-08-912-276-6   |
| 27         | 64    | 94.1  | 68     | 4     | US-08-944-483-10  |
| 28         | 64    | 94.1  | 68     | 4     | US-09-525-397-18  |
| 29         | 64    | 94.1  | 68     | 4     | US-09-566-876-6   |
| 30         | 64    | 94.1  | 68     | 4     | US-09-049-698-20  |
| 31         | 64    | 94.1  | 68     | 4     | US-09-215-818-4   |
| 32         | 64    | 94.1  | 68     | 4     | US-09-065-383-12  |
| 33         | 64    | 94.1  | 68     | 4     | US-09-276-600-3   |
| 34         | 54    | 79.4  | 2544   | 4     | US-09-483-371-1   |
| 35         | 54    | 79.4  | 2606   | 2     | US-08-568-459A-7  |
| 36         | 54    | 79.4  | 2606   | 2     | US-08-487-826B-7  |
| 37         | 54    | 79.4  | 2606   | 4     | US-09-210-288-7   |
| 38         | 54    | 79.4  | 2815   | 3     | US-09-214-564A-1  |

|    |      |      |      |   |                    |                    |
|----|------|------|------|---|--------------------|--------------------|
| 28 | 52.4 | 77.1 | 3327 | 3 | US-08-689-421-26   | Sequence 26, Appli |
| 29 | 52.4 | 77.1 | 3327 | 4 | US-09-389-528-26   | Sequence 26, Appli |
| 30 | 52.4 | 77.1 | 3327 | 4 | US-09-181-827A-26  | Sequence 26, Appli |
| 31 | 42   | 61.8 | 3133 | 4 | US-09-193-069-1    | Sequence 1, Appli  |
| 32 | 40   | 58.8 | 2288 | 2 | US-08-568-459A-5   | Sequence 5, Appli  |
| 33 | 40   | 58.8 | 2288 | 2 | US-08-487-826B-5   | Sequence 5, Appli  |
| 34 | 40   | 58.8 | 2288 | 4 | US-09-210-288-5    | Sequence 5, Appli  |
| 35 | 38.4 | 56.5 | 782  | 4 | US-09-605-785-757  | Sequence 757, App  |
| 36 | 38.4 | 56.5 | 2060 | 4 | US-09-523-849-1    | Sequence 1, Appli  |
| 37 | 37   | 54.4 | 5030 | 2 | US-08-588-201-14   | Sequence 14, Appli |
| 38 | 37   | 54.4 | 5030 | 3 | US-09-169-605-14   | Sequence 14, Appli |
| 39 | 37   | 54.4 | 5030 | 3 | US-08-893-327-14   | Sequence 14, Appli |
| 40 | 32.4 | 47.6 | 915  | 4 | US-09-740-235-10   | Sequence 10, Appli |
| 41 | 30.2 | 44.4 | 533  | 4 | US-09-103-342A-11  | Sequence 11, Appli |
| 42 | 29.8 | 43.8 | 501  | 4 | US-09-605-785-451  | Sequence 451, App  |
| 43 | 29.8 | 43.8 | 501  | 4 | US-09-439-313-451  | Sequence 451, App  |
| 44 | 29.8 | 43.8 | 501  | 4 | US-09-352-616A-451 | Sequence 451, App  |
| 45 | 29.8 | 43.8 | 506  | 4 | US-09-103-542A-5   | Sequence 5, Appli  |

## ALIGNMENTS

RESULT 1  
US-08-964-725-6  
; Sequence 6, Application US/08964725  
; Patent No. 5939265  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/964,725  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5997.US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear



US-08-964-725-6

Query Match 100.0%; Score 68; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCGGACTAGTGTAGCTCGTGCACC 60  
DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCGGACTAGTGTAGCTCGTGCACC 60

QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

## RESULT 2

US-09-071-710-17  
; Sequence 17, Application US/09071710  
; Patent No. 6130043

## GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRAMADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE PROSTATE

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,710

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/850,713

FILING DATE: 02-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6083 US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729

TELEFAX: 847/938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 68 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-071-710-17

Query Match 100.0%; Score 68; DB 3; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCGGACTAGTGTAGCTCGTGCACC 60  
DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCGGACTAGTGTAGCTCGTGCACC 60

QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

## RESULT 3

US-08-883-086-11  
; Sequence 11, Application US/08883086  
; Patent No. 6171787

## GENERAL INFORMATION:

APPLICANT: WILEY, STEVEN

TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL

FOR TREATMENT AND DIAGNOSIS OF DISEASE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/883,086

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Potembski, Priscilla E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 6134.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-937-0378

TELEFAX: 847-938-2623

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 68 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-883-086-11

Query Match 100.0%; Score 68; DB 4; Length 68;

Best Local Similarity 100.0%; Pred. No. 8.2e-16;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCGGACTAGTGTAGCTCGTGCACC 60  
DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCGGACTAGTGTAGCTCGTGCACC 60

QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

## RESULT 4

US-08-912-276-5

; Sequence 5, Application US/08912276

; Patent No. 6183952

; GENERAL INFORMATION:

; APPLICANT: Billing-Medel, Patricia A.

APPLICANT: Cohen, Maurice  
APPLICANT: Colpitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Gordon, Julian  
APPLICANT: Granados, Edward N.  
APPLICANT: Hodges, Steven C.  
APPLICANT: Klass, Michael R.  
APPLICANT: Kratochvil, Jon D.  
APPLICANT: Roberts-Rapp, Lisa  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-912-276-5

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCTCGGAATTCGAGCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGACC 60  
DB 1 ACCTCGGAATTCGAGCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGACC 60  
OY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 5  
US-08-944-483-9  
Sequence 9, Application US/08944483  
Patent No. 6232456  
GENERAL INFORMATION:  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.

APPLICANT: STEWART, KENT D.  
APPLICANT: STROUPE, STEVEN D.  
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
TITLE OF INVENTION: OF THE PROSTATE  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,483  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6183.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-944-483-9

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCTCGGAATTCGAGCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGACC 60  
DB 1 ACCTCGGAATTCGAGCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGACC 60  
OY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 6  
US-09-525-397-17  
Sequence 17, Application US/09525397  
Patent No. 6252047  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE

NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/525,397  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/071,710  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6083.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-525-397-17

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTGAGCTCTGTGACC 60  
Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTGAGCTCTGTGACC 60  
QY 61 CGGGAATT 68  
Db 61 CGGGAATT 68

RESULT 7  
US-09-566-876-5  
Sequence 5, Application US/09566876  
Patent No. 6350583  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Cohen, Maurice  
APPLICANT: Colpitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Granados, Edward N.  
APPLICANT: Klass, Michael R.  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Stephen D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR  
FILE REFERENCE: 6171.US.P1  
CURRENT APPLICATION NUMBER: US/09/566,876  
CURRENT FILING DATE: 2000-05-08  
PRIOR APPLICATION NUMBER: US 08/926,509  
PRIOR FILING DATE: 1997-09-09  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 68

TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-566-876-5

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTGAGCTCTGTGACC 60  
Db 1 AGCTCGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTGAGCTCTGTGACC 60  
QY 61 CGGGAATT 68  
Db 61 CGGGAATT 68

RESULT 8  
US-09-049-698-19  
Sequence 19, Application US/09049698  
Patent No. 6368792  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA A.  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: HAYDEN, MARK  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THE  
TITLE OF INVENTION: USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
TITLE OF INVENTION: TRACT  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/049,698  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,856  
FILING DATE: 31-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6088.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-049-698-19

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATCCGAGCTTGGATCCTAGAGCGCGCGGCGGAGTGTAGTGTGCGACC 60  
|||||  
Db 1 AGCTCGGAATCCGAGCTTGGATCCTAGAGCGCGCGGCGGAGTGTAGTGTGCGACC 60  
|||||  
QY 61 CGGGAATT 68  
|||||  
Db 61 CGGGAATT 68  
|||||

## RESULT 9

US-09-215-818-3  
; Sequence 3, Application US/09215818A  
; Patent No. 6375671  
; GENERAL INFORMATION:  
; APPLICANT: Colipitts, Tracey  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR  
; FILE REFERENCE: 5972 US P2  
; CURRENT APPLICATION NUMBER: US/09/215,818A  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 08/912,276  
; EARLIER FILING DATE: 1997-08-17  
; EARLIER APPLICATION NUMBER: 08/697,105  
; EARLIER FILING DATE: 1996-08-19  
; EARLIER APPLICATION NUMBER: 08/912,149  
; EARLIER FILING DATE: 1997-08-15  
; EARLIER APPLICATION NUMBER: 08/697,106  
; EARLIER FILING DATE: 1996-08-19  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 68  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Unknown  
US-09-215-818-3

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATCCGAGCTTGGATCCTAGAGCGCGCGGCGGAGTGTAGTGTGCGACC 60  
|||||  
Db 1 AGCTCGGAATCCGAGCTTGGATCCTAGAGCGCGCGGCGGAGTGTAGTGTGCGACC 60  
|||||  
QY 61 CGGGAATT 68  
|||||  
Db 61 CGGGAATT 68  
|||||

## RESULT 10

US-09-065-383-11  
; Sequence 11, Application US/09065383  
; Patent No. 6391543  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GORDON, JULIAN  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: HODGES, STEVEN C.  
; APPLICANT: KLAAS, MICHAEL R.  
; APPLICANT: KRATOCHVIL, JON D.  
; APPLICANT: ROBERTS-RAPP, LISA  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STROUPE, STEPHEN D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; FOR DETECTING DISEASES OF THE PROSTATE  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/065,383  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/842,385  
FILING DATE: 23-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6084.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-065-383-11

Query Match 100.0%; Score 68; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATCCGAGCTTGGATCCTAGAGCGCGCGGCGGAGTGTAGTGTGCGACC 60  
|||||  
Db 1 AGCTCGGAATCCGAGCTTGGATCCTAGAGCGCGCGGCGGAGTGTAGTGTGCGACC 60  
|||||  
QY 61 CGGGAATT 68  
|||||  
Db 61 CGGGAATT 68  
|||||

## RESULT 11

US-09-276-600-2  
; Sequence 2, Application US/09276600  
; Patent No. 6465181  
; GENERAL INFORMATION:  
; APPLICANT: Patricia Billing-Medel  
; APPLICANT: Maurice Cohen  
; APPLICANT: Tracey L. Colpitts  
; APPLICANT: Julian Gordon  
; APPLICANT: Edward N. Granados  
; APPLICANT: John C. Russell  
; APPLICANT: Stephen D. Stroupe  
; TITLE OF INVENTION: Reagents and Methods Useful for  
; FILE REFERENCE: 6197 US 01  
; CURRENT APPLICATION NUMBER: US/09/276,600  
; CURRENT FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 68  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Restriction site  
US-09-276-600-2

Query Match 100.0%; Score 68; DB 4; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGAATTCGAGCTTGGATCTCTAGACGCGCGCGGACTAGTACGCTCGACG 60  
 Db 1 AGCTCGAATTCGAGCTTGGATCTCTAGACGCGCGCGGACTAGTACGCTCGACG 60

QY 61 CGGAAAT 58  
 Db 61 CGGAAAT 58

RESULT 12  
 US-08-964-725-7/c  
 ; Sequence 7, Application US/08964725  
 ; Patent No. 5939265  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COHEN, Maurice  
 ; APPLICANT: FRIEDMAN, Paula N.  
 ; APPLICANT: GORDON, Julian  
 ; APPLICANT: HODGES, Steven C.  
 ; APPLICANT: KLASS, Michael R.  
 ; APPLICANT: KRATOCHVIL, Jon D.  
 ; APPLICANT: ROBERTS-RAPP, Lisa  
 ; APPLICANT: RUSSELL, John C.  
 ; APPLICANT: STROUPE, Steven D.  
 ; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 ; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: 100 Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/964,725  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Becker, Cheryl L.  
 ; REGISTRATION NUMBER: 35,441  
 ; REFERENCE/DOCKET NUMBER: 5997.US.P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 847/935-1729  
 ; TELEFAX: 847/938-2623  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 68 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-964-725-7

Query Match 94.1%; Score 64; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-14;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGATTCGAGCTTGGATCTCTAGACGCGCGCGGACTAGTACGCTCGACCGGG 64  
 Db 68 CGGATTCGAGCTTGGATCTCTAGACGCGCGCGGACTAGTACGCTCGACCGGG 9

QY 65 AATT 68  
 Db 8 AATT 5

RESULT 13  
 US-09-071-710-18/c  
 ; Sequence 18, Application US/09071710  
 ; Patent No. 6130043  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BILLING-MEDEL, PATRICIA  
 ; APPLICANT: COHEN, MAURICE  
 ; APPLICANT: COLPITTS, TRACEY L.  
 ; APPLICANT: FRIEDMAN, PAULA N.  
 ; APPLICANT: GORDON, JULIAN  
 ; APPLICANT: GRANDOS, EDWARD N.  
 ; APPLICANT: HODGES, STEVEN C.  
 ; APPLICANT: KLASS, MICHAEL R.  
 ; APPLICANT: KRATOCHVIL, JON D.  
 ; APPLICANT: ROBERTS-RAPP, LISA  
 ; APPLICANT: RUSSELL, JOHN C.  
 ; APPLICANT: STROUPE, STEPHEN D.  
 ; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 ; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE  
 ; NUMBER OF SEQUENCES: 41  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: 100 Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/071,710  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/850,713  
 ; FILING DATE: 02-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Becker, Cheryl L.  
 ; REGISTRATION NUMBER: 35,441  
 ; REFERENCE/DOCKET NUMBER: 6083.US.P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 847/935-1729  
 ; TELEFAX: 847/938-2623  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 68 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-071-710-18

Query Match 94.1%; Score 64; DB 3; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-14;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGATTCGAGCTTGGATCTCTAGACGCGCGCGGACTAGTACGCTCGACCGGG 64  
 Db 68 CGGATTCGAGCTTGGATCTCTAGACGCGCGCGGACTAGTACGCTCGACCGGG 9

RESULT 14  
US-08-883-086-12/c  
; Sequence 12, Application US/08883086  
; Patent No. 6171787  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, STEVEN  
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/883,086  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Porembski, Priscilla E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 6134.US.01  
; TELEPHONE: 847-937-0378  
; TELEFAX: 847-938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-883-086-12

Query Match 94.1%; Score 64; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 2.2e-14;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTAGTGTGAGCTGTGACCGCGG 64  
Db 68 CGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTAGTGTGAGCTGTGACCGCGG 9  
QY 65 AATT 68  
Db 8 AATT 5

RESULT 15  
US-08-912-276-6/c  
; Sequence 6, Application US/08912276  
; Patent No. 6183952  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A.  
; APPLICANT: Cohen, Maurice  
; APPLICANT: Colpitts, Tracey L.  
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Gordon, Julian  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klass, Michael R.  
; APPLICANT: Kratochvili, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa

APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972.US.P1  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-912-276-6

Query Match 94.1%; Score 64; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 2.2e-14;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTAGTGTGAGCTGTGACCGCGG 64  
Db 68 CGGAATTCGAGCTTGGATCTCTAGAGCGCGCGGACTAGTGTAGTGTGAGCTGTGACCGCGG 9  
QY 65 AATT 68  
Db 8 AATT 5

Search completed: February 9, 2003, 22:05:24  
Job time : 5.94273 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model.

Run on: February 9, 2003, 21:14:50 ; Search time 5.24229 Seconds  
(without alignments)  
6148.496 Million cell updates/sec

Title: US-09-099-823-6  
Perfect score: 68  
Sequence: 1 AGCTCGGATTCGAGCTG.....AGCTCGTCCGCGGAAATT 68

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq:  
10: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq:  
12: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq:  
14: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Match | Length | ID | Description        |
|------------|-------|-------|--------|----|--------------------|
| 1          | 68    | 100.0 | 68     | 8  | US-08-926-626-8    |
| 2          | 68    | 100.0 | 68     | 9  | US-10-082-559-5    |
| 3          | 68    | 100.0 | 68     | 9  | US-09-082-236-8    |
| 4          | 68    | 100.0 | 68     | 9  | US-09-104-408-25   |
| 5          | 68    | 100.0 | 68     | 9  | US-10-216-408-17   |
| 6          | 68    | 100.0 | 68     | 10 | US-09-050-516-28   |
| 7          | 68    | 100.0 | 68     | 10 | US-09-276-600-2    |
| 8          | 68    | 100.0 | 68     | 10 | US-09-099-823-6    |
| 9          | 68    | 100.0 | 68     | 10 | US-09-234-717-11   |
| 10         | 68    | 100.0 | 68     | 10 | US-09-850-178-7    |
| 11         | 68    | 100.0 | 68     | 10 | US-09-193-538-8    |
| 12         | 68    | 100.0 | 68     | 10 | US-09-096-883-15   |
| 13         | 68    | 100.0 | 68     | 10 | US-09-250-883-15   |
| 14         | 68    | 100.0 | 68     | 10 | US-09-215-652-17   |
| 15         | 68    | 100.0 | 68     | 10 | US-09-049-695A-6   |
| 16         | 68    | 100.0 | 68     | 10 | US-09-092-297-6    |
| 17         | 68    | 100.0 | 68     | 12 | US-10-025-167-19   |
| 18         | 68    | 100.0 | 474    | 10 | US-09-878-574-4285 |
| 19         | 68    | 100.0 | 690    | 10 | US-09-878-574-4644 |

|      |      |       |      |    |                    |
|------|------|-------|------|----|--------------------|
| 20   | 68   | 100.0 | 698  | 10 | US-09-878-574-4671 |
| 21   | 66.4 | 97.6  | 502  | 10 | US-09-878-574-4207 |
| 22   | 66.4 | 97.6  | 515  | 10 | US-09-878-574-4193 |
| 23   | 64.8 | 95.3  | 507  | 10 | US-09-878-574-4820 |
| c 24 | 64   | 94.1  | 68   | 8  | US-08-926-626-9    |
| c 25 | 64   | 94.1  | 68   | 9  | US-10-082-659-6    |
| c 26 | 64   | 94.1  | 68   | 9  | US-09-082-236-9    |
| c 27 | 64   | 94.1  | 68   | 9  | US-09-104-408-26   |
| c 28 | 64   | 94.1  | 68   | 9  | US-10-216-408-18   |
| c 29 | 64   | 94.1  | 68   | 9  | US-09-050-516-29   |
| c 30 | 64   | 94.1  | 68   | 10 | US-09-276-600-3    |
| c 31 | 64   | 94.1  | 68   | 10 | US-09-099-823-7    |
| c 32 | 64   | 94.1  | 68   | 10 | US-09-234-717-12   |
| c 33 | 64   | 94.1  | 68   | 10 | US-08-850-178-8    |
| c 34 | 64   | 94.1  | 68   | 10 | US-09-193-538-9    |
| c 35 | 64   | 94.1  | 68   | 10 | US-09-230-883-16   |
| c 36 | 64   | 94.1  | 68   | 10 | US-09-096-259-11   |
| c 37 | 64   | 94.1  | 68   | 10 | US-09-215-652-18   |
| c 38 | 64   | 94.1  | 68   | 10 | US-09-049-695A-7   |
| c 39 | 64   | 94.1  | 68   | 10 | US-09-092-297-7    |
| c 40 | 64   | 94.1  | 68   | 12 | US-10-025-167-20   |
| c 41 | 54   | 79.4  | 403  | 10 | US-09-924-035A-590 |
| c 42 | 54   | 79.4  | 2544 | 9  | US-09-957-156-1    |
| c 43 | 54   | 79.4  | 2606 | 9  | US-10-153-273-7    |
| c 44 | 52.4 | 77.1  | 484  | 10 | US-09-878-574-4416 |
| c 45 | 49   | 72.1  | 1029 | 10 | US-09-925-301-39   |

## ALIGNMENTS

RESULT 1  
US-08-926-626-8  
; Sequence 8, Application US/08926626  
; Patent No. US20020035244A1  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STROUSE, STEVEN D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASE OF THE PROSTATE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/926,626  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6158 US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-926-626-8

Query Match 100.0%; Score 68; DB 8; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16; Indels 0; Gaps 0;  
Matches 68; Conservative 0; Mismatches 0;

QY 1 AGCTCGGAATCCGAGCTGGATCTCTAGAGCGCGCGGCGGACTAGTGTGACCTGCGACC 60  
DB 1 AGCTCGGAATCCGAGCTGGATCTCTAGAGCGCGCGGCGGACTAGTGTGACCTGCGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 2  
US-10-082-659-5  
Sequence 5, Application US/10082659  
Patent No. US20020168783A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Cohen, Maurice  
APPLICANT: Colpitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Granados, Edward N.  
APPLICANT: Klass, Michael R.  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Stephen D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR  
TITLE OF INVENTION: DETECTING DISEASES OF THE PROSTATE  
FILE REFERENCE: 6171-US.P1  
CURRENT APPLICATION NUMBER: US/10/082.659  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: 09/566.876  
PRIOR FILING DATE: 2000-05-08  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 68  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-082-659-5

Query Match 100.0%; Score 68; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16; Indels 0; Gaps 0;  
Matches 68; Conservative 0; Mismatches 0;

QY 1 AGCTCGGAATCCGAGCTGGATCTCTAGAGCGCGCGGCGGACTAGTGTGACCTGCGACC 60  
DB 1 AGCTCGGAATCCGAGCTGGATCTCTAGAGCGCGCGGCGGACTAGTGTGACCTGCGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 3  
US-09-092-296-8  
Sequence 8, Application US/09092296  
Publication No. US20020188114A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: KLAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.

APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092.296  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/048,810  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6104.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-092-296-8

Query Match 100.0%; Score 68; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16; Indels 0; Gaps 0;  
Matches 68; Conservative 0; Mismatches 0;

QY 1 AGCTCGGAATCCGAGCTGGATCTCTAGAGCGCGCGGCGGACTAGTGTGACCTGCGACC 60  
DB 1 AGCTCGGAATCCGAGCTGGATCTCTAGAGCGCGCGGCGGACTAGTGTGACCTGCGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 4  
US-09-104-408-25  
Sequence 25, Application US/09104408  
Publication No. US20020188115A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, Patricia A. et al.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0



;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/104,408  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 6122.US.01  
;; FILING DATE: 25-JUN-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Becker, Cheryl L.  
;; REGISTRATION NUMBER: 35,441  
;; REFERENCE/DOCKET NUMBER:  
;; TELEPHONE: 847/935-1729  
;; TELEFAX: 847/938-2623  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 68 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-09-104-408-25

Query Match 100.0%; Score 68; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGGAATTCGAGCTTGATCTCTAGAGCGGCGCGGACTAGTGTGAGCTGTGAC 60  
DB 1 AGCTCGGAATTCGAGCTTGATCTCTAGAGCGGCGGCGGACTAGTGTGAGCTGTGAC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

## RESULT 5

US-10-216-408-17  
; Sequence 17, Application US/10216408  
; Publication No. US20030013159A1

## GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
GRANADOS, EDWARD N.  
KLASS, MICHAEL R.  
RUSSELL, JOHN C.  
STROUPE, STEVEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

TRACT  
FOR DETECTING DISEASE OF THE GASTROINTESTINAL

## NUMBER OF SEQUENCES: 27

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA

ZIP: 60064-3500

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/216,408

FILING DATE: 09-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/959,634

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

;; REGISTRATION NUMBER: 35,441  
;; REFERENCE/DOCKET NUMBER: 6188.US.01  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 847/935-1729  
;; TELEFAX: 847/938-2623  
;; TELEX: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 68 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-10-216-408-17

Query Match 100.0%; Score 68; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGGAATTCGAGCTTGATCTCTAGAGCGGCGGCGGACTAGTGTGAGCTGTGAC 60  
DB 1 AGCTCGGAATTCGAGCTTGATCTCTAGAGCGGCGGCGGACTAGTGTGAGCTGTGAC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

## RESULT 6

US-09-050-516-28

; Sequence 28, Application US/09050516

; Patent No. US20010010904A1

## GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HAYDEN, MARK  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KLASS, MICHAEL R.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

FOR DETECTING DISEASES OF THE GASTROINTESTINAL

TRACT

TITLE OF INVENTION: TRACT

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: IL

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,516

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,855

FILING DATE: 31-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6065.US.P1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:

## INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-050-516-28

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGTGCTGACC 60  
|||||  
DB 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGTGCTGACC 60

QY 61 CGGGAATT 68  
|||||  
DB 61 CGGGAATT 68

## RESULT 7

US-09-276-600-2  
Sequence 2, Application US/09276600  
Patent No. US20010010308A1

## GENERAL INFORMATION:

APPLICANT: Patricia Billing-Medel  
APPLICANT: Maurice Cohen  
APPLICANT: Tracey L. Colpitts  
APPLICANT: Julian Gordon  
APPLICANT: Edward N. Granados  
APPLICANT: John C. Russell  
APPLICANT: Stephen D. Stroupe  
TITLE OF INVENTION: Reagents and Methods Useful for  
TITLE OF INVENTION: Detecting Disease of the Prostate  
FILE REFERENCE: 6397-US-01  
CURRENT APPLICATION NUMBER: US/09/276.600  
CURRENT FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 68  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Restriction site

US-09-276-600-2

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGTGCTGACC 60  
|||||  
DB 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGTGCTGACC 60

QY 61 CGGGAATT 68  
|||||  
DB 61 CGGGAATT 68

## RESULT 8

US-09-099-823-6  
Sequence 6, Application US/09099823  
Patent No. US20020018990A1

## GENERAL INFORMATION:

APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.

APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KASS, MICHAEL R.  
APPLICANT: KRAVOCHVIL, JON D.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: SCHEFFEL, CHRISTI  
APPLICANT: STROUPE, STEPHEN D.  
APPLICANT: YU, HONG  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099.823  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/879,354  
FILING DATE: 20-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6120-US-P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:

## INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-09-099-823-6

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGTGCTGACC 60  
|||||  
DB 1 AGCTCGGAATCCGAGCTTGGATCTCTAGAGCGCGCGCGGACTAGTGTGCTGACC 60

QY 61 CGGGAATT 68  
|||||  
DB 61 CGGGAATT 68

## RESULT 9

US-09-234-717-11  
Sequence 11, Application US/09234717A  
Patent No. US20020034740A1

## GENERAL INFORMATION:

APPLICANT: Patricia Billing-Medel  
APPLICANT: Maurice Cohen  
APPLICANT: Tracey L. Colpitts  
APPLICANT: Paula N. Friedman  
APPLICANT: Julian Gordon  
APPLICANT: Edward N. Granados  
APPLICANT: Steven C. Hodges

APPLICANT: Michael R. Klass  
APPLICANT: Jon D. Kratochvil  
APPLICANT: John C. Russell  
APPLICANT: Stephen D. Stroupe  
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of  
TITLE OF INVENTION: the Breast  
FILE REFERENCE: 6450.US.01  
CURRENT APPLICATION NUMBER: US/09/234.717A  
CURRENT FILING DATE: 1999-01-21  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 11  
LENGTH: 68  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Restriction site  
US-09-234-717-11

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60  
DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 10  
US-09-850-178-7  
Sequence 7, Application US/09850178  
Patent No. US20020034749A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Billing-Medel, Patricia A.  
APPLICANT: Cohen, Maurice  
APPLICANT: Colipitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Russell, John C.  
APPLICANT: Granados, Edward N.  
APPLICANT: Hodges, Steven C.  
APPLICANT: Klass, Michael R.  
APPLICANT: Kratochvil, Jon D.  
APPLICANT: Roberts-Rapp, Lisa  
APPLICANT: Stroupe, Stephen D.  
APPLICANT: Gordon, Julian  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR  
TITLE OF INVENTION: DETECTING DISEASES OF THE BREAST  
FILE REFERENCE: 6251.US.01  
CURRENT APPLICATION NUMBER: US/09/850.178  
CURRENT FILING DATE: 2001-05-07  
PRIOR APPLICATION NUMBER: US 08/972,376  
PRIOR FILING DATE: 1997-11-18  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 68  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Restriction site  
US-09-850-178-7

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60  
DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60

DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 11  
US-09-193-538-8  
Sequence 8, Application US/09193538A  
Patent No. US20020037503A1  
GENERAL INFORMATION:  
APPLICANT: Patricia Billing-Medel  
APPLICANT: Maurice Cohen  
APPLICANT: Tracey L. Colipitts  
APPLICANT: Paula N. Friedman  
APPLICANT: Julian Gordon  
APPLICANT: Edward N. Granados  
APPLICANT: Steven C. Hodges  
APPLICANT: Michael R. Klass  
APPLICANT: Jon D. Kratochvil  
APPLICANT: Lisa Roberts-Rapp  
APPLICANT: John C. Russell  
APPLICANT: Stephen D. Stroupe  
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the  
TITLE OF INVENTION: Breast  
FILE REFERENCE: 6193.US.01  
CURRENT APPLICATION NUMBER: US/09/193.538A  
CURRENT FILING DATE: 1998-11-17  
EARLIER APPLICATION NUMBER: US 08/971,772  
EARLIER FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 68  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Restriction site  
US-09-193-538-8

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60  
DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTGCGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 12  
US-09-250-883-15  
Sequence 15, Application US/09250883  
Patent No. US20020042049A1  
GENERAL INFORMATION:  
APPLICANT: Russell, John  
APPLICANT: Colipitts, Tracey  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
TITLE OF INVENTION: FOR DETECTING DISEASE OF THE BREAST  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/250,883  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/889,316  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6131.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-250-883-15

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGTGCTGACC 60  
DB 1 AGCTCGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGTGCTGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 13  
US-09-096-259-10  
Sequence 10, Application US/09096259  
Patent No. US2002004516A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: GORDON, JULIAN  
APPLICANT: GRANADOS, EDWARD N.  
APPLICANT: HODGES, STEVEN C.  
APPLICANT: KRATOCHVIL, JON D.  
APPLICANT: ROBERTS-RAPP, LISA  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE LONG  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/096,259

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/049,183  
FILING DATE: 11-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6113.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-096-259-10

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGTGCTGACC 60  
DB 1 AGCTCGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGTGCTGACC 60  
QY 61 CGGGAATT 68  
DB 61 CGGGAATT 68

RESULT 14  
US-09-215-652-17  
Sequence 17, Application US/09215652  
Patent No. US2002004516A1  
GENERAL INFORMATION:  
APPLICANT: Patricia Billing-Medel  
APPLICANT: Maurice Cohen  
APPLICANT: Tracey L. Colpitts  
APPLICANT: Paula N. Friedman  
APPLICANT: Julian Gordon  
APPLICANT: Edward N. Granados  
APPLICANT: Steven C. Hodges  
APPLICANT: Michael R. Klass  
APPLICANT: Jon D. Kratochvil  
APPLICANT: Lisa Roberts-Rapp  
APPLICANT: John C. Russell  
APPLICANT: Stephen D. Stroupe  
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the  
TITLE OF INVENTION: Breast  
FILE REFERENCE: 6192.US.F1  
CURRENT APPLICATION NUMBER: US/09/215,652  
EARLIER FILING DATE: 1998-12-16  
EARLIER APPLICATION NUMBER: US 08/998,496  
EARLIER FILING DATE: 1997-12-26  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 68  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Restriction site  
US-09-215-652-17

Query Match 100.0%; Score 68; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.4e-16;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGAATTCGAGCTTGGATCTCTAGAGCGCGCCGCGACTAGTGTGCTGACC 60

DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGGCGCGGACTAGTGTGCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

RESULT 15

US-09-049-695A-6  
 : Sequence 6, Application US/09049695A  
 : Patent No. US20020137904A1  
 : GENERAL INFORMATION:  
 : APPLICANT: BILLING-MEDEL, PATRICIA A.  
 : APPLICANT: COHEN, MADRICE  
 : APPLICANT: COLPITTS, TRACEY L.  
 : APPLICANT: FRIEDMAN, PAULA N.  
 : APPLICANT: HAYDEN, MARK  
 : APPLICANT: KLAAS, MICHAEL R.  
 : APPLICANT: ROBERTS-RAPP, LISA  
 : APPLICANT: RUSSELL, JOHN C.  
 : APPLICANT: STROUPE, STEPHEN D.  
 : TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 : TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
 : TITLE OF INVENTION: TRACT  
 : NUMBER OF SEQUENCES: 25  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Abbott Laboratories  
 : STREET: 100 Abbott Park Road  
 : CITY: Abbott Park  
 : STATE: IL  
 : COUNTRY: USA  
 : ZIP: 60064-3500  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: DOS  
 : SOFTWARE: FASTSEQ for Windows Version 2.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/049.695A  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/828,845  
 : FILING DATE: 31-MAR-1997  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Becker, Cheryl L.  
 : REGISTRATION NUMBER: 35,441  
 : REFERENCE/DOCKET NUMBER: 6066-US.P1  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 847/935-1729  
 : TELEFAX: 847/938-2623  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 68 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : US-09-049-695A-6

Query Match 100.0%; Score 68; DB 10; Length 68;  
 Best Local Similarity 100.0%; Fred. No. 4.4e-16;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGGCGCGGACTAGTGTGCTGCGACC 60  
 DB 1 AGCTCGGAATTCGAGCTTGGATCCTCTAGAGCGGCGCGGACTAGTGTGCTGCGACC 60  
 QY 61 CGGGAATT 68  
 DB 61 CGGGAATT 68

Search completed: February 9, 2003, 22:08:37  
 Job time : 6.24229 secs

Mon Feb 10 11:12:14 2003

us-09-099-823-6.rst

Page 1

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2003, 22:05:30 ; Search time 189.022 Seconds  
(without alignments)  
5826.269 Million cell updates/sec

Title: US-09-099-823-6

Perfect score: 68

Sequence: 1 AGCTCGAATTCGAGCTTG.....AGCTCTGACCCGGAATT 68

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pin:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fut:\*

23: em\_gss\_fun:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 54.4  | 80.0        | 600    | 14 | BM960199    |
| 2          | 54    | 79.4        | 128    | 9  | AU036326    |
| 3          | 54    | 79.4        | 595    | 14 | BM960119    |
| 4          | 54    | 79.4        | 597    | 14 | BM960836    |
| 5          | 54    | 79.4        | 600    | 14 | BM960064    |
| 6          | 54    | 79.4        | 756    | 17 | AG011933    |

|    |      |      |     |    |          |
|----|------|------|-----|----|----------|
| 7  | 53   | 77.9 | 191 | 13 | BI703139 |
| 8  | 53   | 77.9 | 626 | 13 | BI843511 |
| 9  | 53   | 77.9 | 644 | 17 | AG012264 |
| 10 | 53   | 77.9 | 699 | 17 | AG011969 |
| 11 | 53   | 77.9 | 733 | 17 | AG011861 |
| 12 | 52   | 76.5 | 602 | 14 | BM960255 |
| 13 | 50.8 | 74.7 | 604 | 14 | BM959632 |
| 14 | 50.8 | 74.7 | 597 | 14 | BM960676 |
| 15 | 49.8 | 73.2 | 599 | 14 | BM960731 |
| 16 | 47.8 | 70.3 | 600 | 14 | BM959996 |
| 17 | 47.8 | 70.3 | 608 | 14 | BM960089 |
| 18 | 47   | 69.1 | 727 | 17 | AG011876 |
| 19 | 42.4 | 62.4 | 637 | 17 | AG012462 |
| 20 | 42   | 61.8 | 409 | 13 | BI807825 |
| 21 | 42   | 61.8 | 582 | 13 | BI809564 |
| 22 | 38   | 55.9 | 251 | 9  | AL362705 |
| 23 | 33.6 | 49.4 | 330 | 10 | AW976016 |
| 24 | 33.6 | 49.4 | 347 | 10 | AW971301 |
| 25 | 33.6 | 49.4 | 412 | 10 | AW973221 |
| 26 | 33.6 | 49.4 | 436 | 10 | AW973170 |
| 27 | 33.6 | 49.4 | 438 | 10 | AW973753 |
| 28 | 33.6 | 49.4 | 465 | 10 | AW979187 |
| 29 | 33.6 | 49.4 | 472 | 10 | AW974074 |
| 30 | 33.6 | 49.4 | 476 | 10 | AW968194 |
| 31 | 33.6 | 49.4 | 484 | 10 | AW979229 |
| 32 | 33.6 | 49.4 | 486 | 10 | AW972891 |
| 33 | 33.6 | 49.4 | 489 | 10 | AW971397 |
| 34 | 33.6 | 49.4 | 498 | 10 | AW970083 |
| 35 | 33.6 | 49.4 | 499 | 10 | AW969651 |
| 36 | 33.6 | 49.4 | 501 | 10 | AW971736 |
| 37 | 33.6 | 49.4 | 504 | 10 | AW970095 |
| 38 | 33.6 | 49.4 | 538 | 10 | AW971324 |
| 39 | 33.6 | 49.4 | 544 | 10 | AW973097 |
| 40 | 33.6 | 49.4 | 550 | 10 | AW970568 |
| 41 | 33.6 | 49.4 | 551 | 10 | AW974890 |
| 42 | 33.6 | 49.4 | 566 | 10 | AW968338 |
| 43 | 33.6 | 49.4 | 581 | 10 | AW974890 |
| 44 | 33.6 | 49.4 | 594 | 10 | AW970992 |
| 45 | 33.6 | 49.4 | 595 | 10 | AW968212 |

#### ALIGNMENTS

RESULT 1

BM960199

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM960199 600 bp mRNA linear EST 18-MAR-2002  
c1ha301s Ascidian hemocytes cDNA library Ciona intestinalis cDNA,  
mRNA sequence.

BM960199.1 GI:19543626

EST.

Ciona intestinalis.

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 600)

Shida,K., Terajima,D., Satake,M., Kawazoe,Y. and Kasuya,A.

Sequence tags expressed in hemocytes of Ciona intestinalis

Unpublished (2002)

Contact: Masanobu Satake

Department of Molecular Immunology

Institute of Development, Aging and Cancer, Tohoku University

Seiryomachi 4-1, Aoba-ku, Sendai 980-8575, Japan

Tel: 81-22-717-8477

Fax: 81-22-717-8482

Email: satake@idac.tohoku.ac.jp.

Location/Qualifiers

1. 600

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone\_lib="Ascidian hemocytes cDNA library"

/cell\_type="hemocytes"



Db 16 AGCTTGATCCTCTAGAGCGCGCCGCGACTAGTGTGAGCTGCTGCGACCGGGAATT 69

## RESULT 5

BH960064

LOCUS 600 bp mRNA linear EST 18-MAR-2002  
 DEFINITION cihaj398 Ascidian hemocytes cDNA library ciona intestinalis cDNA,  
 mRNA sequence.

ACCESSION BH960064

VERSION BH960064.1 GI:19543491

KEYWORDS EST.

SOURCE Ciona intestinalis.

ORGANISM Ciona intestinalis

REFERENCE 1 (bases 1 to 600)  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Cloniidae; Ciona.

AUTHORS Shida,K., Terajima,D., Satake,M., Kawazoe,Y. and Kasuya,A.

TITLE Sequence tags expressed in hemocytes of Ciona intestinalis

JOURNAL Unpublished (2002)

COMMENT Contact: Masanobu Satake

Department of Molecular Immunology

Institute of Development, Aging and Cancer, Tohoku University

Seiryomachi 4-1, Aoba-ku, Sendai 980-8575, Japan

Tel: 81-22-717-8477

Fax: 81-22-717-8482

Email: satake@idac.tohoku.ac.jp.

FEATURES

Location/Qualifiers

1..600

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone.lib="Ascidian hemocytes cDNA library"

/cell.type="hemocytes"

/dev\_stage="adult"

/note="Vector: pZL1; Site 1: EcoRI"

BASE COUNT 149 a 112 c 143 g 194 t 2 others

ORIGIN

Query Match 79.4%; Score 54; DB 14; Length 600;

Best Local Similarity 100.0%; Pred. No. 5.9e-06;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 AGCTTGATCCTCTAGAGCGCGCCGCGACTAGTGTGAGCTGCTGCGACCGGGAATT 68

Db 16 AGCTTGATCCTCTAGAGCGCGCCGCGACTAGTGTGAGCTGCTGCGACCGGGAATT 69

## RESULT 6

AG011933

LOCUS

DEFINITION Homo sapiens genomic DNA, 21q region, clone: f61E7X13, genomic  
 survey sequence.

ACCESSION AG011933

VERSION AG011933.1 GI:3395752

KEYWORDS GSS.

SOURCE Homo sapiens DNA, clone:f61E7X13.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 756)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

TITLE Homo sapiens genomic DNA, chromosome 21q

JOURNAL Published Only in DataBase (1998)

REFERENCE 2 (bases 1 to 756)

AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (06-AUG-1998) Masahira Hattori, Kitasato University,  
 Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,  
 Sagamihara 228, Japan (E-mail:hattori@egc.ims.u-tokyo.ac.jp,  
 Tel:0427-78-9732, Fax:0427-78-9561)

FEATURES

Location/Qualifiers

1..756

/organism="Homo sapiens"

/db\_xref="taxon:9606"

Query Match

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/chromosome="21"

/map="21q"

/clone="f61E7X13"

BASE COUNT 145 a 142 c 153 g 180 t 136 others

## ORIGIN

Query Match 79.4%; Score 54; DB 17; Length 756;

Best Local Similarity 100.0%; Pred. No. 6.1e-06;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 AGCTTGATCCTCTAGAGCGCGCCGCGACTAGTGTGAGCTGCTGCGACCGGGAATT 68

Db 72 AGCTTGATCCTCTAGAGCGCGCCGCGACTAGTGTGAGCTGCTGCGACCGGGAATT 125

## RESULT 7

B1703139

LOCUS

DEFINITION B1703139 191 bp mRNA linear EST 18-SEP-2001  
 fr95f02.xl zebrafish adult olfactory Danio rerio cDNA clone 5002106  
 3' similar to SW:CATACAMJE Q59296 CATALASE ;, mRNA sequence.

ACCESSION B1703139

VERSION B1703139.1 GI:15665768

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 191)

AUTHORS Clark,M., Johnson,S.L., Lebrach,H., Lee,R., Li,F., Marra,M., Eddy

S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Willie,T., Underwood

K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,

Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,

Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.

and Wilson,R.

TITLE Washo zebrafish EST Project 1998

JOURNAL Unpublished (1998)

COMMENT Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrfish@wustl.edu

cDNA Library Preparation: John Ngai cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center. DNA distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:

www.rzp.de)

Possible reversed clone: similarity on wrong strand

Seq primer: T7 from Gibco

High quality sequence stop: 181.

Location/Qualifiers

1..191

/organism="Danio rerio"

/db\_xref="taxon:9555"

/clone="5002106"

/clone.lib="zebrafish adult olfactory"

/sex="mixed"

/tissue.type="olfactory rosettes"

/dev\_stage="adult"

/lab\_host="D10Hb (Gibco BRL)"

/note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI; This

is a directionally cloned cDNA library from adult

zebrafish olfactory epithelium."

BASE COUNT 39 a 52 c 51 g 49 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 16 GCTTGGATCCTCTAGAGCGCGCCGCGACTAGTGTAGCTGTCTGACCGCGGAATT 68  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 GCTTGGATCCTCTAGAGCGCGCCGCGCGACTAGTGTAGCTGTCTGACCGCGGAATT 53  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

## RESULT 8

BI843511

LOCUS

DEFINITION ft30f01.x1 zebrafish adult olfactory Danilo rerio cDNA clone 5283193  
 3' similar to SW:CAVA\_CAME\_Q59296 CATALASE ; mRNA sequence.

ACCESSION BI843511

VERSION BI843511

KEYWORDS EST

SOURCE zebrafish.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
 ; Cyprinidae; Danio.

REFERENCE

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy  
 , K., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood  
 , K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,  
 Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,  
 Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.  
 and Wilson, R.

TITLE

JOURNAL

COMMENT

WashU Zebrafish EST Project 1998  
 Unpublished (1998)  
 Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrafish@wustl.wustl.edu

CNA Library Preparation: John Ngai CNA Library Arrayed by:  
 Matthew Clark. DNA Sequencing by: Washington University Genome  
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,  
 Missouri (web address: www.genomesystems.com) (email contact:  
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
 (web address: www.resgen.com) (email contact: info@resgen.com) and  
 Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:  
 www.rzpd.de)

Possible reversed clone: similarity on wrong strand

Seq primer: T7 from Gibco

High quality sequence stop: 200.

FEATURES

source

Location/Qualifiers  
 1..626  
 /organism="Danio rerio"  
 /db\_xref="taxon:7955"  
 /clone="5283193"  
 /sex="mixed"  
 /tissue="olfactory adult olfactory"

/dev\_stage="adult"

/lab\_host="D10BD (Gibco BRL)"

/note="Vector: pSPORI1; Site\_1: NotI; Site\_2: SalI; This  
 is a directionally cloned cDNA library from adult  
 zebrafish olfactory epithelium."

BASE COUNT 132 a 175 c 179 g 118 t 22 others

ORIGIN

Query Match 77.9%; Score 53; DB 13; Length 626;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GCTTGGATCCTCTAGAGCGCGCCGCGCGACTAGTGTAGCTGTCTGACCGCGGAATT 68

|||||

Db 1 GCTTGGATCCTCTAGAGCGCGCCGCGCGACTAGTGTAGCTGTCTGACCGCGGAATT 53

|||||

## RESULT 9

AG012264

LOCUS

DEFINITION Homo sapiens genomic DNA, 21q region, clone: B355D16X37, genomic  
 survey sequence.

ACCESSION AG012264

VERSION AG012264

KEYWORDS GSS

SOURCE

ORGANISM

DEFINITION Homo sapiens genomic DNA, 21q region, clone: B355D16X37, genomic  
 survey sequence.

ACCESSION AG012264

VERSION AG012264

KEYWORDS GSS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

1..644

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="21"

/map="21q"

/clone="B355D16X37"

BASE COUNT 132 a 131 c 143 g 154 t 84 others

ORIGIN

Query Match 77.9%; Score 53; DB 17; Length 644;

Best Local Similarity 98.1%; Pred. No. 1.2e-05;

Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACCTTGGATCCTCTAGAGCGCGCCGCGCGACTAGTGTAGCTGTCTGACCGCGGAATT 68

|||||

Db 63 ACCTTGGATCCTCTAGAGCGCGCCGCGCGACTAGTGTAGCTGTCTGACCGCGGAATT 116

|||||

## RESULT 10

AG011969

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

1..699

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="21"

/map="21q"

/clone="B175P11A94"

BASE COUNT 137 a 130 c 152 g 166 t 114 others

ORIGIN

Query Match 77.9%; Score 53; DB 17; Length 699;

Best Local Similarity 98.1%; Pred. No. 1.2e-05;  
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 68  
|||||  
Db 64 ACCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 117  
|||||

## RESULT 11

AG011861

LOCUS

AG011861 733 bp DNA linear GSS 07-FEB-1999  
DEFINITION Homo sapiens genomic DNA, 21q region, clone: B14B21N15, genomic survey sequence.

ACCESSION

AG011861

VERSION

AG011861.1

KEYWORDS

GSS

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

JOURNAL

Published Only in Database (1998)

REFERENCE

Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

JOURNAL

Submitted (06-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail: hattori@jst.ims.u-tokyo.ac.jp, Tel: 0427-78-9732, Fax: 0427-78-9561)

FEATURES

Location/Qualifiers

1..733

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="21"

/map="21q"

/clone="B14B21N15"

BASE COUNT

183 a 162 c 142 g 218 t 28 others

ORIGIN

Query Match

Best Local Similarity 77.9%; Score 53; DB 17; Length 733;

Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 68  
|||||Db 65 ACCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 118  
|||||

## RESULT 12

BM960255

LOCUS

BM960255

DEFINITION

ciba4F20S Ascidian hemocytes cDNA library Ciona intestinalis cDNA, mRNA sequence.

ACCESSION

BM960255

VERSION

BM960255.1

KEYWORDS

EST

SOURCE

Ciona intestinalis.

ORGANISM

Ciona intestinalis

REFERENCE

Shida, K., Terajima, D., Satake, M., Kawazoe, Y. and Kasuya, A.

JOURNAL

Sequence tags expressed in hemocytes of Ciona intestinalis

COMMENT

Unpublished (2002)

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Fax: 81-22-717-8482

Email: satake@dac.tohoku.ac.jp.

FEATURES Location/Qualifiers  
1..602  
/organism="Ciona intestinalis"  
/db\_xref="taxon:7719"  
/clone\_lib="Ascidian hemocytes cDNA library"  
/cell\_type="hemocytes"  
/dev\_stage="adult"  
/note="Vector: pZLI; Site 1: EcoRI"

BASE COUNT 224 a 103 c 103 g 169 t 3 others  
ORIGIN

Query Match

Best Local Similarity 76.5%; Score 52; DB 14; Length 602;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTTGGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 68  
|||||Db 20 CTTGGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 71  
|||||

## RESULT 13

BM959632

LOCUS

BM959632

DEFINITION

ciba10F2S Ascidian hemocytes cDNA library Ciona intestinalis cDNA, mRNA sequence.

ACCESSION

BM959632

VERSION

BM959632.1

KEYWORDS

EST

SOURCE

Ciona intestinalis.

ORGANISM

Ciona intestinalis

REFERENCE

Shida, K., Terajima, D., Satake, M., Kawazoe, Y. and Kasuya, A.

JOURNAL

Sequence tags expressed in hemocytes of Ciona intestinalis

COMMENT

Unpublished (2002)

Contact: Masanobu Satake

Department of Molecular Immunology

Institute of Development, Aging and Cancer, Tohoku University

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Tel: 81-22-717-8477

Fax: 81-22-717-8482

Email: satake@dac.tohoku.ac.jp.

FEATURES Location/Qualifiers

1..597

/organism="Ciona intestinalis"

/db\_xref="taxon:7719"

/clone\_lib="Ascidian hemocytes cDNA library"

/cell\_type="hemocytes"

/dev\_stage="adult"

/note="Vector: pZLI; Site 1: EcoRI"

BASE COUNT

198 a 110 c 122 g 165 t 2 others

ORIGIN

Query Match

Best Local Similarity 74.7%; Score 50.8; DB 14; Length 597;

Matches 52; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 AGCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 68  
|||||Db 16 AGCTTGATCCTCTAGAGCGCGCGGACTAGTGTGCTGCGACCGGGAATT 69  
|||||

## RESULT 14

BM960676

LOCUS

BM960676

DEFINITION

ciba4F21S Ascidian hemocytes cDNA library Ciona intestinalis cDNA, mRNA sequence.

ACCESSION

BM960676

VERSION

BM960676.1

KEYWORDS

EST

SOURCE

Ciona intestinalis.

ORGANISM

Ciona intestinalis

